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Result
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1: /cgn2_6/ptodata/2;

2: /cgn2_6/ptodata/2;

3: /cgn2_6/ptodata/2;

4: /cgn2_6/ptodata/2;

5: /cgn2_6/ptodata/2;

6: /cgn2_6/ptodata/2;
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/backfiles1.pep:*
                                                                        PCT-US95-01219-44
US-08-561-521-10
US-08-595-01219-10
US-08-290-592E-17
PCT-US95-10053-14
PCT-US96-09448-17
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US-08-646-265A-99
                     US-08-232-081B-8
US-09-025-769B-36
US-09-025-769B-59
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US-08-561-521-13
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Sequence 12, Appl
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Sequence 14, Appl
Sequence 10, Appl
Sequence 10, Appl
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19, Appl
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472	472	473	473	473	473	473	473	473	473	474	481	481	484.5	484.5	484.5	484.5	484.5
72.1	72.1	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.4	73.4	73.4	74.0	74.0	74.0	74.0	74.0
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US-08-483-389-86	US-08-482-882-86	US-08-475-680-53	US-08-714-017-53	US-08-720-420A-53	US-08-483-932-53	US-08-473-503-53	US-08-487-113D-53	US-08-483-389-53	US-08-482-882-53	US-08-836-561-74	US-08-964-690-23	-202	US-08-603-024-18	US-08-452-164A-19	US-08-253-877C-19	US-08-436-717-112	US-08-137-117D-112
Sequence 86,	Sequence 86,				Sequence 53,					Sequence 74,		Sequence 23,		Sequence 19,	Sequence 19,	Sequence 112	Sequence 112
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ALIGNMENTS

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US-08-561-521-11
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Best Local Similarity
                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VIA-4
NUMBER OF ASQUENCES: 45
ADDRESSED: Townsend and Townsend Knourie and Crew
ADDRESSEE: Townsend and Townsend Knourie and Crew
                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                NAME: Smith, William L. REGISTRATION NUMBER: 30,223 REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/561,521 FILING DATE:
                                                                                                                                                                                                                                                       TELEFAX:
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100.0%;
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Score 655; DB 2;
Pred. No. 1.8e-58;
                Length 123;
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PCT-US95-01219-11
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Best Local Similarity 100.0%; Pred Mo. 1.8e-58;
Matches 123; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 11:
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APPLICANY: Jones, S. Tarran
TITIE OF INVENTION: Humanized Antibodies Against Leukocyte
TITIE OF INVENTION: Absolon Molecule VIA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/1
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 25-JAN-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGYYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend Khourie and Crew
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                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                        1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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; Sequence 17, Application PC/TUS9501219
                          PCT-US95-01219-17
                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORREY/ACENT INFORMATION:
NAME: SMITH, WILLIAM L.
REGISTRATION NUMBER: 30,223
REGERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELECHOME: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend Khourie and Crew
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Humanized Antibodies Ag
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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STATE: California
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                                                                                                                                                                                                     80 DPKFQGRYTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 139
                                                                                                                                                                                                                                                    61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 655; DB 2; Length 142; 100.0%; Pred. No. 2.2e-58;
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Patent No. 5840299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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SEQUENCE CHARACTERISTICS:
LENCTH: 142 amino acids
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                                                                                                                                                   GENERAL INFORMATION:
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FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
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             APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Loger, Olivier J.
APPLICANT: Jones, S. Terran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COPERATOR S-5-1-1
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                            121 VSS 123
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Local Similarity 100.0%; Pred. No. 2.2e-58;
hes 123; Conservative 0; Mismatches 0; Indels
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One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                           Application US/08561521
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, MOLECULE TYPE: protein US-08-561-521-9
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MEDIUM TYPE: Floppy
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
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LENGTH: 123 amino acids
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                                                                                                                                                                 TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/561,521
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COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                    CITY:
                                                                 COUNTRY:
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                                                                                                                                  ADDRESSEE:
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                                                                                                  San Francisco
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APPLICANT: Jones, S.
TITLE OF INVENTION:
TITLE OF INVENTION:
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PATRIC TOTAL 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/185,269A
                                                                                                 CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                               APPLICATION NUMBER: US/08/561,521 FILING DATE:
                                                                                                                                              COMPUTER:
                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
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TELEPHONE: 415-543-9600
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ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DPKFOGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 60
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FILING DATE: 25-JA
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One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                             Leger, Olivier J.
Saldanha, Jose
Jones, S. Tarran
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                                                                                                                                                          Floppy disk
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                                                                                                                                                                                                                                                                                                                                    Humanized Antibodies Against Leukocyte
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PCT-US95-01219-4
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         TELEPHONE: 415-543-960
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application PC/TUS9501219 GENERAL INFORMATION:
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Best Local Similarity 82.6%; Pred, No. 2.6e-47;
Matches 100; Conservative 11; Mismatches 10; Indels
SEQUENCE CHARACTERISTICS:
                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                               FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
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SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte PITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                            NAME: Smith, William L. REGISTRATION NUMBER: 30,223
                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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Saldanha, Jose
Jones, S. Tarran
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415-543-5043
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TOPOLOGY: linear
US-08-871-488A-19
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                                                                                                        TELEFAX: (206) 682-60 IN NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT BIND TO THE TITLE OF INVENTION: ANTIGEN BOUND BY ANTIBODY NR-LU-13 AND THEIR USE IN TITLE OF INVENTION: PRETARGETING METHODS
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MEDIUM TYPE: Floppy
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                                                                                       SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
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                                                                                                                                                                              NAME: Sharkey Ph.D., Richard G
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 69002
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0
FILING DATE: 09-JUN-1997
                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                  STRANDEDNESS
                                                    TYPE:
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                                                                   LENGTH:
                                                    amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rees, Anthony R.
                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Henry, Andrew H.
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                                                                                                                            (206)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jan T.
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; Patent No. 6214973
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                                        Matches 103; Conservative
                                                       Query Match 79.8%;
Best Local Similarity 83.7%;
                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 132:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: RESHAPED HUMAN ANTIBOTITLE OF INVENTION: MEDULLOBLASTOMA CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                                                 MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 09-SE
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                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: WO PCT/JP94/01763
                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                            NAME:
1 OVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                    amino acid
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3000 K Street, N.W., Suite 500
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VENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SATO, Koh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OHTOMO, Toshihiko
                                                                                                                                                                                                                                                                               (202)672-5399
                                                                                                                                                                     linear
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                                                         Score 523; DB 4; Length 117; pred. No. 2.6e-45;
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                                                                                                                                                                     Matches 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 5-23...
APPLICATION NUMBER: JP 5-23...
APPLICATION NUMBER: JP NOV1993
APPLICATION NUMBER: JP NOV1993
NAME: MEGCER, HATOID C.
NAME: MEGCER, HATOID C.
NAME: MEGCER, HATOID C.
15, 256
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
LENGTH: 136 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
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PRIOR APPLICATION DATA
APPLICATION NUMBER: NO PCT/JP94/01763
FILING DATE: 19-CCT-1994
PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
80 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 133
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TITLE OF INVENTION: MEDULLOBLASTOWA CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OHTOMO, TO
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                           61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                            Y Match 79.8%; Score 523; DB 4; Length 136; Local Similarity 83.7%; Pred. No. 3.1e-45;
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                                                                                 20 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 79
                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                           TYPE:
                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQKLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                      amino acid
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                Mismatches
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DP 64

1 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

RESULT

137 VSS 139

121 VSS 123

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; MOLECULE TYPE: protein US-08-646-265A-109
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      Matches 103; Conservative
                      Best Local Similarity
                                        Query Match
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                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
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APPLICANT: OHTOMO, Toshihiko
                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 09-SEP-19
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANY: SATO, KOH
APPLICANY: SATO, KOH
APPLICANY: TUTLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
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                                                                                                                                          TYPE:
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                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                           TELEFAX:
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                                                                                                                                                                                                                                                                                          NAME: WEGNER, Harold C
REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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STREET: Washington
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                                                                                                                                       amino acid
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                                                                                                                                                         269 amino acids
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                                                                                                                          linear
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IBM PC compatible
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19-OCT-1994
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79.8%; Score 523; DB 4; Length 269; 83.7%; Pred. No. 6.9e-45; ative 4; Mismatches 10; Indels
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PCT-US95-01219-13 : Sequence 13, Application PC/TUS9501219 ; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unary Match 78.6%; Score 515; DB 2; Length 119;
Best Locat Similarity 82.9%; Pred, No. 1.7e-44;
Matches 102; Conservative 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 13:
                                           APPLICANT:
                                                              APPLICANT:
  TITLE OF INVENTION:
                        APPLICANT:
                                                                               APPLICANT:
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REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanize
TITLE OF INVENTION: Adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier J.
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                                                                                                                                                                                                                                                                  121 VSS 123
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                                                                                                                                                                                                                                                                                                61 SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYFGS----GSNYWGQGTLVT 116
                                                                                                                                                                                                                                                                                                                                       61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQRLEWMGWINAGNGNTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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                   : Bendig, Mary M.
: Leger, Olivier J.
: Saldanha, Jose
: Jones, S. Tarran
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Humanized Antibodies Against Leukocyte
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                                                                                                                                                                                                                             ; Patent No.
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                                                                                                                                                                                                                                                Sequence 12,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 102;
                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                     TITLE OF INVENTION: Humanized Antibodies Ag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                     117 VSS 119
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    STATE:
                STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                          121 VSS 123
                                               ADDRESSEE: Townsend and Townsend Khourie and Crew
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                                                                                                                                                                                                                                                                                                                                                                                                                       61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0 FILING DATE: 25-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWNGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Smith, William REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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California
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Leger, Olivier J.
Saldanha, Jose
Jones, S. Tarran
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One Market Plaza, Steuart Tower, Suite 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-1995
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                                                                                                                 Humanized Antibodies Against Leukocyte
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Pred. No. 1.7e-44;
5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15270-14
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COUNTRY: USA

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; STRANDEDNESS: single
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-08-561-521-12
Search completed: July 9, 2002, 15:39:04 Job time: 30 sec
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APPLICATION NUMBER: US/08/186,269A

FILING DATE: 23-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: SMIth, WILLIAM L.

RESISTRATION NUMBER: 30.223

RESISTRATION NUMBER: 30.223

RESISTRATION NUMBER: 30.223

RESISTRATION NUMBER: 15270-14

TELEPOMPUNICATION INFORMATION:

TELEPOMPUNICATION INFORMATION:

TELEPOMPUNICATION 10.00

TELEPOMPUNICATION 10.00

TELEPOMPUNICATION 10.00

SEQUENCE CHARACTERISTICS:

LENGTH 119 anino acids

TYPE: amino acids

TYPE: amino acids
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Best Local Similarity 82.9%; Pred, No. 3.3e-44;
Matches 102; Conservative 4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: TEM PO compatible

DEBATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: PALENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/561.521

FILING DATE:

CLASSIFICATION: 424
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                          117 VSS 119
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                                                                                                                                                                                                                    61 DPKPGGRYTIADTSASTAYMELSSLRSEDTANYYCARECYYGYZAMYWGOGTLYF 120
61 SQKFQGRYTIADTSASTAYMELSSLRSEDTANYYCARECYYGS---GSNYWGOGTLYF 116
61 SQKFQGRYTIADTSASTAYMELSSLRSEDTANYYCARGGYYGS---GSNYWGOGTLYF 116
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
OM protein - protein search, using sw model
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Aun on: July 9, 2002, 15:38:34; Search

July 9, 2002, 15:38:34 : Search time 28,27 Seconds (Without alignments) 60:293 Willion cell updates/sec

Title: US-09-010-377-1
Perfect score: 562

Periect score: 304
Sequence: 1 DIOMTOSPESLEASVGDRVT.....YCLQVDNLWTEGOGTKVEIK 106

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Gapop 10.0 , Gapext 0.5 Searched: 283138 seqs, 96089334 residues

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

Database: PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	90	7	6	5	4	ω	N	-		Result
412	412.5	413.5	414	414.5	415.5	418.5	419.5	419.5	421.5	424.5	426	429.5	429.5	435.5	439.5	439.5	439.5	440	440.5	443	443.5	•	446.5	452	463.5	478	479	488		Score
73.3	73.4	73.6	73.7	73.8	73.9	74.5	74.6	74.6	75.0	75.5	75.8	76.4	76.4	77.5	78.2	78.2	78.2	78.3	78.4	78.8	78.9	78.9	79.4		82.5	5	85.2	86.8		Query
106	108	108	124	131	109	123	108	108	108	125	107	127	110	108	108	107	107	94	107	103	129	108	107	97	125	106	104	104		Length DB
2 PC2397	2 B4904/	1 KIHUSW	2 540336	2 \$40352	2 831998	2 540331	1 KIHURY	1 KIHUAG	1 KIHULY	2 840333	2 \$36275	2 \$40367	2 \$44118	2 139154	1 KIHUAU	2 PL0271	2 PL0269	2 E33730	2 PL0272	2 526332	2 S52789	1 KIHURE	2 PL0270	2 PH1064	2 509365	2 C33936	2 S26329	2 S26330	:	B IĐ
difficience coxin	Topology Pr	ig Kappa chain	ig kappa	ig kappa chain	Id vappa cuari	Id kappa	19 Kappa	I vappa chain	adday 51	ig kappa chain	Ig Iamoud Chain	To addon for	to sappa chain	Eddby fit	ig Kappa Chain	19 Kappa charu	addex 51	is kappa caa	Ig kappa	authir fil	1g xappa	lg kappa		Light	Ig Kappa	g kappa cua	Ig Kappa	Ig kappa		Description

ALIGNMENTS

RESULT S26330

RESULT 2 \$26329 chain V region - mouse ig kappa chain V region - mouse (Speciles: Mus musculus (house mouse) (Clacession: \$26329 R. Stark S.E.; Caton A.J. 1991 J. Exp. Med. 174, 613-624, 1991 J. Exp. Med. 174, 613-624, 1991 A. Title: Antibodies that are specific for a single amino acid interchange in a protei A. Title: Antibodies that are specific for a single amino acid interchange in a protei A. Reference number: \$26309; MUID:91341421 A. Recession: \$26309; MUID:91341421 A. Accession: \$26309; MUID:91341421 A. Accession: \$26309; MUID:913614421 A. Cression: \$2630	Query Match Best Local Similarity 85.8%; Fred. No. 1.6e-35; Best Local Similarity 85.8%; Fred. No. 1.6e-35; Matches 89; Conservative 8; Mismatches 7; Indels 0; Gaps 0; Matches 199; Conservative 8; Mismatches 7; Indels 0; Gaps 0; Qy 1 DIQMTQSPSSLSASVGCRVTITCKTSODINKYLAMYQOTPKARRILLHYTSALOPGIPS 60 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	C;Species: Mis misroulus (noise mouse) C;Dates: [3-,4n-1995 **sequence_revision 13-Jan-1995 **text_change 20-Jun-2000 C;Datession: \$2630 C;Accession: \$2630 R;Stark, S.E.; Caton, A.T. 1. Exp. Med. 174, 613-624, 1991 A;Title: Antibodies that are specific for a single amino acid interchange in a proteil A;Title: Antibodies that are specific for a single amino acid interchange in a proteil A;Reference number: \$26309; MUID:91341421 A;Reference interval and a single amino acid interchange in a proteil A;Reference interval and a single amino acid interchange in a proteil A;Residues: preliminary A;Molecule type: mRNA A;Residues: 1-104 <8TA> A;Cross-references: EMBLIX59185; NID:952316; PIDN:CAA41895.1; PID:91334063 A;Cross-references: EMBLIX59185; NID:952316; PIDN:CAA41895.1; PID:91334063 C;Superfamily: immunoglobulin bomology <imm></imm>
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C:Superfamily: immunoglobulin V region; immunoglobulin homology C:Keywords: heterotetramer; immunoglobulin F:33-107/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                                                                              A: Molecule type: DNA
A: Residues: 1-125 <FED>
                                                                                                                                                                                                                                                                                                                                                                       A:Title: Direct evidence for intrastrand DNA inversion of kappa immunoglobulin gene segn A:Reference number: S09365; MUID:90098844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 17, 9797-9809, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: S09365
R; Feddersen, R.; van Ness, B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A:Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene A:Reference number: A33936; MUID:89282831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-106 < MEE>
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C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C:Accession: C39336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
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                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 85.1%; Score 478; DB 2; Best Local Similarity 83.0%; Pred. No. 1.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
               * 18 DIOMTOSPSSLSASLGGKYTITCKASODINKYIAWYOHKPGKGPRLLIHYTSTLOPGIPS 77
                                                         1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGRDYSFSISNLDPEEIATYYCLQYDSLYTFGGGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYLAWYQHKPGKGPRLLIHYTSTLQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIOMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMTQSPSSLSASLGGKYTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIOMTQSPSSLSASYGDRYTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                        89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;88
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                    82.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Mismatches
                                                                                                                                    Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 479; DB 2; Length 104; Pred. No. 9.7e-35;
                                                                                                               Mismatches
                                                                                                                                 2.5e-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 106;
                                                                                                                                                       DB 2; Length 125;
                                                                                                               10;
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                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                           F;24-34/Region: complementarity-determining 1
                                                                                                                                                                                                                                                                                              F;57-88/Region: framework 3
                                                                                                                                                                                                                                                                                                                 F;50-56/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                               F; 35-49/Region:
                                                                                                                                                                                                                                                                                                                                                                                            F;16-90/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                              F;1-23/Region: framework
                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: PL0270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: PL0231; MUID: 90111618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-90/Domain: immunoglobulin homology <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: PL0270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-97 <TIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A: Accession: PH1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Date:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 light chain V region (clone 202.54) ~ mouse (fragment)
C:Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                Matches
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61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGRDYTFTISSLQPEDIATTYCLQYDNLWTF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RESGSGSGRDYSESISNLEPEDIATYYCLQYDNLETF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RESGSGSGRDYTETISSLQPEDIATVYCLQYDNLW-TEGOGTKVEIK 106
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                                                                                                                                                                                                                                                                                                                                               framework 2
                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin homology <IMM>
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                       79.4%; Score 446.5; DB 2
79.4%; Pred. No. 6.4e-32;
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                                                                                                                                    11; Mismatches
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Pred. No. 1.9e-32;
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                                                                                                                                 10; Indels
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A; Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
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C.Specides: Ms musculis (house mouse)
C.Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N. J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
1 DIOMTOSPCSLSASLGDKVTTTCRTSQDISKNMAWYOHKAGKGPRLLIWYTSTLOPGIPS 60
                                                                    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                                                                                                                        DB 2; Length 107;
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                                                                                                                                         Gaps
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lg kappa chain v region - human (fragment)
C;Species: Homo saplens (man)
C;Decies: 19-May-1955 sequence_revision 21-Jul-1995 *text_change 21-Jan-2000
C;Accession: $52789
R;Rocca, A.; Khamilchi, A.A.; Touchard, G.; Mougenol, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the EMBL Data Library, March 1995
A;Description: Light Chain V region gene usage restriction and peculiarities in myeloma-A;Roceronce number: $52789
A;Accession: $52789
                                                                                                                              A:Cross-references: BMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keyvords: heterotetramer; immunoglobulin
F:38-112/Domain: Immunoglobulin homology <IMM>
                                                                                                                                                                                                                                             A: Molecule type: mRNA
A: Residues: 1-129 < ROC>
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A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap cases, and disulfide bonds: In some cases, such as 1gA and 1gM, the subunits associate into la c:Superfamily: immunoglobulin v region; immunoglobulin homology

C:Superfamily: immunoglobulin v region; immunoglobulin homology

E:6-90/Domain: immunoglobulin homology </mm>
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A.Reference number: A9032; MUID:7603968
A.Connents: annotation, X-ray crystallography, 2.0 angstroms
C.Comment: This is a Bence Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A: Note: the C region of this chain has the Inv (1,2) marker R: Epp. O.; Lattman, E.E., Schiffer, M.: Huber, R.: Palm, W. Hlochemistry 14, 4943-4952, 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975
A:Title: Die Primærstruktur einer kristallinen monoklonalen Immunglobulin-L-Kette vom vollstændige Aninosæeurosequenz des Proteins.
A:Reference number: A91663; MUID:76023758
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C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A91663; A01873
R:Palm, W.: Hilschmann, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Cross-references: GDB:136264
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A: Residues: 1-108 <PAL>
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              Matches
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                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTDYTFTISSLQPEDIATYYCOOYQSLPYTFGOGTKLQI 106
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          Conservative
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81.1%;
                            78.9%; Score 443.5; DB 2
79.4%; Pred. No. 1.4e-31;
          :0

 9; Mismatches

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   Mismatches
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                                                  DB 2; Length 129;
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   Indels
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Gaps
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                  F;98-107/Region:
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F;50-56/Region: complementarity-determining F;57-88/Region: framework 3 F;89-97/Region: complementarity-determining
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A:Title: Anti-DNA entibodies from autoimmune mice arise by clonal expansion and somat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain v region (anti-DNA, 6B8VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Accession: PL0272 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
                                                                                                                                                F;24-34/Region: complementarity-determining 1
                                                                                                                                                                                                                                                C;Superfamity: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: PL0231; MUID:90111618
A; Accession: PL0272
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                                                                                                                                                                                                                      F;1-23/Region: framework 1
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                                                                                                                                                                                                                                                                                                                                                A: Molecule type: mRNA
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A; Residues: 1-103 <ST2>
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C;Date: 19:Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C;Accession: $26332; $26331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S26331
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A:Note: the sequence of residues 1-8 and the corresponding nucleic acid sequence are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
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174, 613-624, 1991
                                                                                                                          framework 2
framework 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V region (anti-DNA, 3E12VK) - mouse (fragment)
c;Species: Mus musculus (house mouse)
c;Bate: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
c;Accession: pL0269
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, P.
T. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Reference number: PL0231; MUID:90111618
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C;Species: Mus musculus (house mouse)
C;Datte: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
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A: Molecule type: mRNA
A: Rosidues: 1107 <SHL>
C: Superfamily: immunoglobulin v region: immunoglobulin homology c: Superfamily: immunoglobulin v region: immunoglobulin c: Keywords: heterotetramer: immunoglobulin r: 1-23/Region: framework 1 immunoglobulin homology <immorphysical complementarity-determining 1 r; 35-49/Region: complementarity-determining 2 r; 35-49/Region: complementarity-determining 2 r; 57-58/Region: complementarity-determining 3 r; 89-97/Region: complementarity-determining 3 r; 89-107/Region: framework 4
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A; Residues: 1-94 <LAW>
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A;Accession: E33730
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E33730
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Best Local :
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Local Similarity 86.2%;
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Pred. No. 2e-31;
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Query Match

Score 439.5;

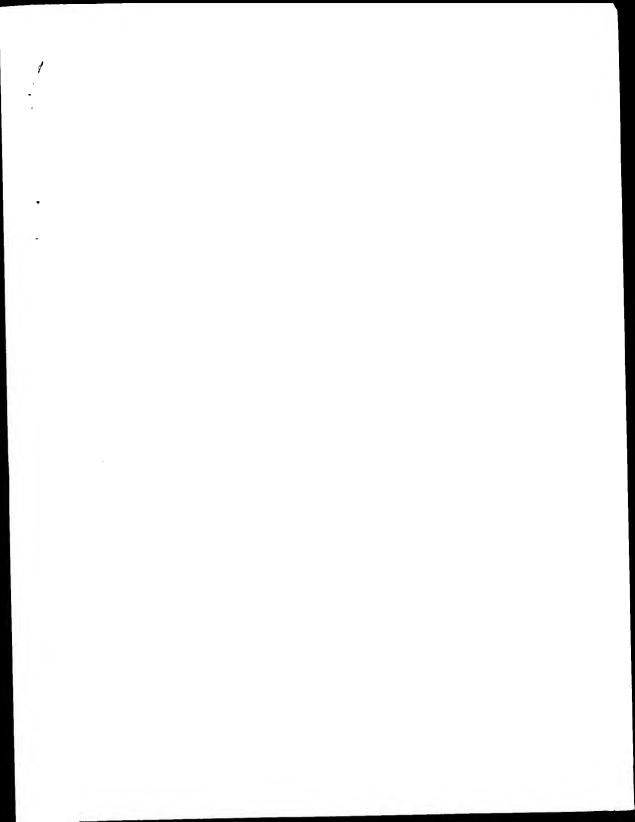
DB 2;

Length 107;

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F;50-56/Region:
F;57-88/Region:
F;89-97/Region:
F;98-107/Region:
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C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lg kappa chain V-I region (Au) - human
C:spacies Homo sapiens (man)
C:bate: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000
C:Accession, Api53, Ab163, B02573
E:Schlechi, H: Hischmann New 353 345-270 1077
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A; Residues: 1-107 <SHL>
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A;Accession: PL0271
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J. Exp. Med. 171, 265-297, 1990
                                                                                                                                                                        A; Note: the C region of this chain has the Inv (3) marker
A; Note: the C region of this chain has the Inv (3) marker
A; Note: the C region of this chain, P.M.; Lattman, E.E.; Schwager, P.; S
Biophys. Struct. Weeh. 1, 139-146, 1975
Biophys. Struct. Weeh. 1, 139-146, 1975
A; Title: The structure determination of the variable portion of the Bence-Jones prote
                                                                                                                                                                                                                                                                                                                                                                                                                     Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ.
A; Title: Chemical modification of the carboxyl groups of protein substrates enhances
                            R;Steiner, V.; Chang, J.Y. FEBS Lett. 222, 6-10, 1987
                                                                                        \lambda:Contents: annotation; X-ray crystallography \lambda:Note: the structure of the V region was determined by molecular replacement methods
                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 1-108 <SCH>
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A;Accession: A91653
                                                                                                                                            A; Reference number: A90729; MUID:77022433
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Local Similarity 78.5%;
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10; Mismatches 12
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C:SUperfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetrimmer: immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 kappa chain (BRE) - human (fragment)
C:Species: Homo saplens (man)
C:Date: Ji-May-1996 #soquence_revision 31-May-1996 #text_change 21-Jan-2000
C:Accession: 139154
R:Schormann, M.; Murcell, J.R.; Liepnieks, J.J.; Benson, M.D.
Proc. Matl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
A:Reference number: 139154; MUID:9600304
A:Recession: 139154
A:Recession: 139154
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A:Molecule type: mRNA
A:Residues: 1-108 <RES>
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A:Map Position:2012.0121
A:Map Position:2012.0121
C:Complex:ion:Immonstabulin heterotetramer subunit consists of two identical light (kap C:Complex:ion:Immonstabulin such as 1gA and 1gM, the subunits associate into la him of the immunoglobulin V region; hamunoglobulin homology the immunoglobulin C:Superfemily: immunoglobulin V region; hamunoglobulin homology complex: immunoglobulin file:90/Domain: immunoglobulin homology citMxo
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A:Contents: annotation
C:Comment: This is a Bence Jones protein.
C:Genetics:
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hes 85; Conservative 9; Mismatches 12; Indels |
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OM protein - protein search, using sw model Run on: July 9, 2002, 15:39:44; Search time 15:81 Seconds (without alignments) 259:660 willion cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Title: Perfect score:

US-09-010-377-1
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1 DIOMTOSPSSLSASVGDRVT......YCLQYDNLWTFCQGTKVEIK 106

Scoring table: Gapop 10.0 , Gapext 0.5 BLOSUM62

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ύ 4 Ο πυσό ώ Ο π	COUS: THIS IHURE: IFBB-84. FFBB-84. 19_03506; 19_003596; 19_1; 10; 1, 10; 1, 10; 10; 10; 10; 10; 10; 10; 10; 10; 10;	MEDILINE, MEDILINE, PUDMED-809329; Palim W., Hilschmann N.; Palim W., Palim Y., P	STANDAR Rel. 01, Rel. 01, Rel. 38, n V-I reg (14uman, Ch heria; Pr
	IS A BENCE-JONES PROTEIN. MHC. Bence-Jones protein; 3D-structure. FRAMEBORK-1. COMPLEMENTARITY-DETERMINING-1. FRAMEBORK-2. FRAMEBORK-3. COMPLEMENTARITY-DETERMINING-2. FRAMEBORK-3. FRAMEBORK-3. COMPLEMENTARITY-DETERMINING-3. FRAMEBORK-4.	MBB: PubMed-809329; Mmann N: Tructure of a crystalline monoclonal immunoglobulin tructure of a crystalline monoclonal immunoglobulin tructure of a crystalline monoclonal immunoglobulin talin, subgroup i (Bence-Jones protein Reil); isolation zation of the tryptic peptides; the complete amino ocid a protein; a contribution to the elucidation of the protein; a contribution to the elucidation of the z. physiol. Chem. 356:167-191(1975). Z. physiol. Chem. 356:167-191(1975). SCRAPHY (2.0 ANGSTROMS). BE: E. Schiffer M., Huber R., Palm W.; BE: Tructure of a dimer composed of the variable portions structure of a dimer composed of the variable portions structure of a dimer composed of the variable portions structure of a dimer composed of the variable portions structure of a dimer composed of the variable portions structure of a dimer composed of the variable portions structure of a dimer composed of the variable portions structure of a dimer composed of the variable portions structure of a crystalline and the variable portions structure of a composed of the variable portions structure of a composed of the variable portions structure of a composed of the variable portions structure of a composed of the variable portions structure of a composed of the variable portions structure of a composed of the variable portions structure of a composed of the variable portions	ARD; PRT: 108 AA. Created) Last sequence update) Last annotation update) egion Rei. Chordata: Craniata: Vertebrata: Buteleostomi; Primates: Catarrhini; Hominidae; Homo.

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Mammalia; Eutheria; Primates;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
19 kappa chain Y-I region AU.
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-- MISCELLANDOUS: THE C REGION OF THIS CHAIN HAS

-- MISCELLANDOUS: THIS IS A BENCE-JONES PROTEIN.
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                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS
                                                                                                                                                          MISCELLANEOUS: THE STRUCTURE OF THE
                                                                                                 A01862; K1HUAU.
; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFSGSGSGRDYTFTISSLOPEDIATYYCLOYDNL-WTFGQGTKVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESGSGSGTDYTETISSLQPEDIATYYCQQYQSLPYTEGQGTKLQI
                                                          PF00047; ig; 1.
; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                     Struct. Mech. 1:139-146(1975)
                                                                            IPR003596; Ig_v.
                                                                                        IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57
57
n V region;
1 23
24 34
35 49
50 56
57 88
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108
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81.1%;
                                                Bence-Jones protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
 FRAMEWORK-3.
          COMPLEMENTARITY-DETERMINING-2
                   COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 443.5; DB 1
Pred. No. 5.9e-40;
                                       FRAMEWORK - 1
                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9E8143E1188BCE2A CRC64;
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                                                                                                                                                                                                          Colman P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                  108
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                                                                                                                                                  THE KNOWN STRUCTURE OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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Best Local 9
Matches 85
                                                 Matches
                                                                  Query Match
Best Local
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DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin V region DOMAIN 1 23
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Scand. J. Immunol. 5:677-684(1976).

-I MISCELLANBOOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS SPECIAL MITH THOUSE OF THE HUMAN POM V-III KAPPA CHAIN.
MITH HHIGH IT SHARES CERETAIN IDIOTYPIC DETERMINANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo Sapiens (Human).

Phikarvota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Phikarvota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                            SEQUENCE
                                                                                                                                                                              NON_TER
                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Capra J.D., Klapper D.G., 
"Complete amino acid sequence of the variable domains of 
IGM anti-gamma_globulins (Lay/Pom) with shared idiotypic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KV1M_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=77038198; PubMed=824717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain V-I region Lay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P01605;
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                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;

    -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLOBULIN ACTIVITY. ; A01871; K1HULY.
     DIQMTQSPSSLSASVGDRYTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFSGGGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIQMTOSPSSLSASVGDRVTITCOASODISDYLNWYQQKPGKAPKLLIYDASNLESGVPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P01607; 1REI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85;
                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003006; Ig_MHC
                                                                                                                                                            108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108
                                                 Conservative
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                                                                                                                                                            11834
                                                                  75.0%;
75.0%;
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Pred. No. 1.5e
B; Mismatches
                                                               Score 421.5;
Pred. No. 1.
                                                                                                                                                                                                                                                 COMPLEMENTARITY - DETERMINING - 3
                                                                                                                                                                                                                                                                  FRAMEWORK - 3
                                                                                                                                                                                                                                                                                         COMPLEMENTARITY - DETERMINING - 2
                                                                                                                                                                                                                                                                                                           FRAMEWORK-2
                                                                                                                                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4. BY SIMILARITY.
                                                                                                                                                                                                                      FRAMEWORK - 4
                                                                                                                                                                                                                                                                                                                                                         FRAMEWORK-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                            739993A95431434A CRC64
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                                                 Mismatches
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                                                                     1.2e-37;
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                                                                                          DB 1;
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                                                    13,
                                                    Indels
                                                                                       Length
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                                                                                            108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       two
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                                                 3,
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                                              Gaps
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DIQMTQSF8SLSVSVGDRVTITCQASQNVNAYLNMYQQKFGLAFKLLIYGASTREAGVPS
RESGSGSGRDYTFT1SSLQPEDIATYYCLQYDNLM--TFGQGTKVEIK 106

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                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 82
                                                                                 p01608;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
1g kappa chain V-I region Roy.
                                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
 Hilschmann N.;
                                                                  Eukaryota; Metazoa;
                                                                                                                                                             LEWON'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. BIOI. Chem. 244:350-3560(1969).

1. MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
1. MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Itani K., Shinoda T., Putnam F.W.;
"The amino acid sequence of a kappa type Bence-Jones protein.
complete sequence and the location of the disulfide bridges."
         MEDLINE-68362076; PubMed-5595110
                       SEQUENCE
                                                      Mammalia; Eutheria; Primates;
                                                                             Homo sapiens (Human)
                                                                                                                                                 KV1P_HUMAN
                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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SMART; SM00406; TGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A01861; K1HUAG. HSSP; P01607; IREI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-69234734; PubMed-4893682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KV1A_HUMAN
P01593;
                                            NCBI_TaxID-9606
                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR003006;
InterPro: IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin V region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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                                                                                                                                                                                                                              61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                                                                                                   1 DIQMTQSPSSLSASVGDRVTITCQASQDINHYLNWYQQGPKKAPKILIYDASNLETGVPS 60
                                                                                                                                                                                                                                                                        1 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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    Last sequence update)
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                                                                  Chordata;
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Pred. No. 2e-37;
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COMPLEMENTARITY-DETERMINING-2
                                                                                                                                                                                                                                                                                                                                                                                                               FRAMEWORK - 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAMEWORK -
                                                      Catarrhini; Hominidae; Homo
                                                                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                 PRT;
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Best Local Similarity
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P80362;
01-NOV-1995
01-NOV-1995
15-JUL-1999
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SEQUENCE
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DOMAIN
"Characterization and preliminary crystallographic data on the VL-
related fragment of the human kI Bence Jones protein Wat.";
                                                                        MEDLINE=81267384; PubMed=6167731; Stevens F.J., Westholm F.A., Pana
                                                                                                                                                                   Biochemistry 33:14848-14857(1994).
                                                                                                                                                                                         "Comparison of crystal structures of two homologous proteins:
structural origin of altered domain interactions in immunoglobulin
light-chain dimers.";
                                                                                                                                                                                                                                                              Huang D. B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz Solomon A., Stevens F.J., Schiffer M.;
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region WAT.
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DOMAIN 24 34
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(In) Franck F., Shugar D. (eds
                                               Popp R.A., Solomon A.;
                                                                                                                          SEQUENCE OF 1-35
                                                                                                                                                                                                                                                                                                             MEDLINE-95086080; PubMed-7993911;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hilschmann
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    I - MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)

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                                                                                                                                                                                                                                                                                                                                   AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
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                                                                           Westholm F.A., Panagiotopoulos N., Schiffer
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Pred. No. 2e-37
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SMART; SM00406; iGv
Tmmunoglobulin V re
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                                                                                                                                                                                                                                                                                                                                                                    Kappa-Type (Bence-Jones protein Scw.), II: The chymotryptic
and the complete amino acid sequence.",
Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
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15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Scw.
Homo sapiens (Human)
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P01609;
21-JUL-1986 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-75059271; PubMed-4435756;
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                       ВΥ
                                                        COMPLEMENTARITY-DETERMINING-3
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COMPLEMENTARITY-DETERMINING-2.
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                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through
between the Swiss Institute of Bioinformatics and the EL
the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                   Klobeck H.G., Combriato G., Zachau H.G.; "Immunoglobulin genes of the kappa light chain lymphoid cell lines are closely related."; Nucleic Acids Res. 12:6995-7006(1984).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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15-JUL-1999 (Rel.
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13-AUG-1987
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IPR003596; Ig_v.
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COMPLEMENTARITY-DETERMINING-3
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COMPLEMENTARITY-DETERMINING-1
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RESERVE OCCUPATION
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21-JUL-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KV1D_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pfam; pr00047; ig; l.
smarr; sm00406; iGv; l.
immunoglobulin V region; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 0), Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -! - MISCELLANEOUS:
          Anino held sequence of the Fv region of a human monoclonal 19M (protein MEN) with antibody activity against 3.4 ppruvylated galactose in Klebsheila polysaccharides K30 and K33."
                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro: IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
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                                                    Conl F., Franglone B.;
                                                                 MEDLINE-83273707; PubMed-6410398;
                                                                                                                              Eukaryota; Metazoa; Chordata;
                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                P01610;
                                                                                                                                                                                                                            KA18 HOWAN
 Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983)
                                                                               SEQUENCE
                                                                                                       NCBI_TaxID=9606;
                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                           Ig kappa chain V-I region WEA.
                                                                                                                                                                                                                                                                                                                                                                                                                 TOCA I
                                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISSLZPBBFATYYCQQYNTFFTEGPGTKVDIK 106
                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGRDYTFTISSIQPEDIATTYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kappa chain V-I region CAR.
                                                                                                                                                                                                                                                                                                                                                1 DIOMTOSPSSLSASVGDRVTITCKTSODINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESCSCSGTDETLTISSLOPEDSATYYCOOSYSTLITEGOGTRLEIK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESGSGSGRDYTFTISSLOPEDIATYYCLQ-YDNLWTFGQGTKVEIK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A01864; KIHUAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P80362; 1WTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blochem. 49:377-391(1974)
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11703 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 72.8%;
                                                                                                                                                                                                                                                                                                                                                                                                        20;
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Pred. No. 2.5e-36
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                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                108 AA
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                                                                                                                       Hominidae;
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Best Local
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SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A01876; K1HUWE. HSSP; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- MISCELLANDOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
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                                                                                                                                                                                                   subgroups.';
HOPPE-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).

INSCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER

-:- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        P01600;
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                KV1H_HUMAN
                                                                                                                                                                                                                                                     chain of subgroup I (Bence-Jones Protein Hau):
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-9606;
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                                                                                                                            Pfam; PF00047; ig:
SMART; SM00406; IG
                                                                                                                                                                              HSSP; P80362; LWTL.
                                                                                                                                                                                                                                                                             Watanabe S., Hilschmann N.;
                                                                                                                                                                                                                                                                                           MEDLINE-71032830; PubMed-4097974;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                                                                                                         A01868; K1HUHU.
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                                                                                                                            ig; 1.
IGv; 1
                                                                                                    region;
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                         107
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88
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                                                                                                                  Bence-Jones protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Mismatches
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Pred. No. 2.8e-36
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                                                                FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2
                                                                                        COMPLEMENTARITY - DETERMINING - 1
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                           FRAMEWORK-4
                                                     FRAMEWORK-3
                                                                                                    FRAMEWORK - 1
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KV1F_HU
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                                                                                                                                                                                                                                                                         Query Match
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SMART: SMO0406; for 1.
Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Biochemistry 9:3188-3196(1970).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gall W.E., Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=71064027; PubMed-4923144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFIDE BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochemistry 9:3155-3161(1970).
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"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        " MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER. " MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The covalent structure of a human gamma G-immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=71064023; PubMed-5489770;
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15-JUL-1999 (Rel. 38, Last annotation update)
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P01598;
                                 6T RFSGSGSGRDYTFTISSLQPEDIATYYCLQYD-NLWTFGQGTKVEIK 106
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                                                                                     DIOMTQSPSTLSASVGDRVTITCRASQSINTWLAWYQQKPGKAPKLLMYKASSLESGVPS 60
                                                                                                                                          DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
              DIQMTQSPSSLSASVGDRVTITCRASQSISSYLSWYQQKPGKAPQVLIYAASSLPSGVPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01, Created)
                                                                                                                                                                                                                                                                                                                                                   11788 MW;
                                                                                                                                                                                                                               70.7%; Score 397.5; DB 70.1%; Pred. No. 4e-35;
                                                                                                                                                                                                                                           70.1%;
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72.9%;
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Pred. No. 1.:
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NAMOH_NAMAN
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immunoglobulins. I. Protein & with the Inv(3) allotypic marker.";
J. Hiochem. 7:1277-1296(1975)
-!- MISCELLANBOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                             "Comparative structural studies on the light chains of human
                                                                                          Shinoda T.
                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                             Ig kappa chain V-I region Ka.
Homo sapiens (Human).
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                                                                                                       MEDLINE=76189985; PubMed=818073;
                                                                                                                                  SEQUENCE
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SMART; SM00406; IG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mol. Immunol. 23:73-78(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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13-AUG-1987
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InterPro;
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es 75; Conserv
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IPR003596; Ig_v.
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70.1%;
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FRAMEWORK-4.
BY SIMILARITY.
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21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
19 kappa chain vi region DEE.
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InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGv; I.
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HSSP; P01607; 1REI.
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SMART: SM00406; IGv: 1.
Immunoglobulin V region; Bence-Jones protein.
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InterPro; IPR003006; Ig_MHC
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Score 388.5; DB 1; Length 108; Pred. No. 3.6e-34;
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FRAMEWORK-4.
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Search completed: July 9, 2002, 15:45:57 Job time: 373 sec

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Minimum DB seq length: 0
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 DIQMTQSPSSLSASVCDRVTITCKTSQDINKYMAMYQQTPGKAPRLLIHYTSALQPGIPS 60 	Query Match 76.2%; Score 428.5; DB 4; Length 108; Best Local Similarity 76.6%; Pred. No. 1.1e-40; Matches 82; Conservative 8; Mismatches 16; Indels 1; Gaps	SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;	TER 100	SMART; SM00406; IGv; 1.	InterPro; IPR003596; Ig_v. Pfam; PF00047; iq; 1.			AF035037; AAD56273.1;	Tetus."; Clim. Jamunol. Jamunomathol. 87:184-192/1998)	"Myosin-reactive autoantibodies in rheumatic carditis and normal		Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,	MEDLINE=98277139; PubMed=9614934;	SEQUENCE FROM N.A.				hordata.	Homo saniens (Human)	(FRAGMENT).		(TrEMBLrel. 13,	01-MAY-2000 (TrEMBLrel. 13, Created)		Q9UL77 PRELIMINARY; PRT; 108 AA.	09uL77	RESULT 1

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01-DEC-2001 (TREMBLIE). 19, Last sequence update)
01-DEC-2001 (TREMBLIE). 19, Last annotation update)
ANTI-CEA 79 SINGLE CHAIN FV FRAGMENT (FRAGMENT).
Mus musculus (Mouse).
Eukaryota:
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Q921A6;
Q1-DEC-2001
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Homo sapiens (Human).
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01-DEC-2001 (TIEMBLIE1. 19, Last sequence update)
01-DEC-2001 (TIEMBLIE1. 19, Last annotation update)
aNTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOSIOBULIN KAPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and generation of a single-chain FV molecule (SCFV)."; wol. Cells 7:816.812(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98170165; PubMed-9509426; Chung J.H., Choi I.H., Lee S.C Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.C Yi K.S., Sah P.G., Ryu S.H., Chung H.K.; "Cloning and characterization of cDNAs encoding VH and VL of "Cloning and characterization of cDNAs encoding VH and VL of
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                               antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
                                                                                             Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.M.
*Molecular analysis of polyreactive monoclonal antiodies from
rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
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                                                                                                                                                                                                                                                                                                                                                                                                                                 RFSGSGSGRDYSFSISNLEPEDIATYYCLHYDNLHTFGGGTKLELK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIELTOSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRSAHTLHIYIQPGIPS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U88067; AAB48044.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
241 AA;
  107
107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26086 MW;
  11520 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 418;
Pred. No. '
                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0276887248E9C771 CRC64;
                                                                                                                                                                                                                                                                                                                                                     PRT;
    4BB43E9C5B577F16 CRC64;
                                                                                                                                                                                                                                                                                                                                                     107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; DB 11;
4.5e-39;
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                                                                                                                                                                                                                                                                           LIGHT CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murinae; Mus.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ol-MAY-2000 (TrEMBLrel. 13, Created)
Ol-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Ol-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                             09/UBA1;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003006; Ig_MHC InterPro; IPR003596; Ig_v. Pfam; PF00047; Ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9UL70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UL70
                                                                                                                                                            Q9UL81
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P01607; 1REI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fetus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Young D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wu X., Liu B., Van der Merwe P.L., Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                       NCBI_TaxID=9606;
                                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                 Eukaryota; Metazoa;
                                                            Homo sapiens (Human)
                                                                                          MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE
                                                                            (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTLTFGGGTKVEIK 106
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                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                  1 DIOMTOSPSSLSASVGDRYTITCKTSQDINKYNAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                                                                                                                                                        RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL·WTFGQGTKVEIK 106
                                                                                                                                                                                                                           RESGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTEGPGTKLEIK 107
                                                                                                                                                                                                                                                                             DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunol. Immunopathol. 87:184-192(1998)
AF035044; AAD56280.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                108 AA;
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                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                11633 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.7%;
                                                                                                                                                                                                                                                                                                                                             72.3%;
                                                   Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.
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                                                                                                                                                                                                                                                                                                                                             Score 406.5; DB 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 4.8e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                B7BEDC3E41FCCA37 CRC64;
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                                                                                                                                                             107
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                                                                                                                                                                                                                                                                                                                                                           DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berney
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                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGION
                                                                                             REGION
                                                                                                                                                                                                                                                                                                                                                             108;
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SEQUENCE FROM N.A.

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Best Local
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Best Local
                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                         01 MAY-2000 (TIERHELFE! 13, Last Sequence update)
01 DEC-2001 (TIERHELFE! 19, Last ennotestion update)
MYOSIN-REACTIVE IMMUNOCLOBULIN LIGHT CHAIN VARIABLE RECION
                                                                                                                                                                                                                                                                                                                                                                                                       Q9UL79;
                                                                                                                                                                            Pfam; PF00047; 1g; 1.
                                                                                                                                                                                                                                                                                                                    Homo spolens (Human),
Eukaryota: Metazoa: Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                    InterPro: IPR003006; Ig_MHC InterPro: IPR003596; Ig_v.
                                                                                                                                                                                                                                          fetus.
                                                                                                                                                                                                                                                              Young D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam: PF00047; lg; 1.
SMART: SM00406; IGV; 1.
                                                                                                                                                                                                                                               "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                             NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003596; Ig_v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF035033; AAD56269.1; -. HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                        (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003006; Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fetus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Young D.C.;
      61
                          61
                                                            1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                          -MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RESGSGSGTDFTLTISGLQAEDFATYYCQQSYSALTFGPGTKVDIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                     6
  RFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSFPPTFGQGTKVEIK 107
                       RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                          DIVMTQSPSLLSASTGDRVT1SCRMSQG1SSYLAWYQQKPGKAPELL1YAASTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIOMTOSPSSLSASVGDRVTITCRASOSISNYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60
                                                                                                                                                                                                          AF035035; AAD56271.1; P01607; 1REI.
                                                                                                                                                                                                                                1mmuno1
                                                                                                                                                                  SM00406; IGV; 1.
                                                                                                                                                                                                                                                                    Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunol. Immunopathol. 87:184-192(1998)
                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                     108 AA;
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                                                                                                                                                108
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                            . Immunopathol. 87:184-192(1998).
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                                                                                                                                     11787 MW;
                                                                                             68.6%;
72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11501 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.38;
71.78;
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                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                            Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 395; DB 4;
Pred. No. 6.7e-37;
                                                                                                                                     DB5845F19724FB4E CRC64
                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 070549FDE0754748 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                108
                                                                                             .9e-36;
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                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 107
                                                                                                    Length 108;
                                                                                  Indels
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                                                                                  1:
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Q91WS9
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Q9R1A5
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Query Match
Best Local Similarity
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Best Local
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                                       Hypothetical protein.
NON_TER 1
SEQUENCE 233 AA; 2
                                                                                        Strausberg R.;
                                                                                                                                                                                                                091WS9
                                                                                                                                                                                                                           Q91WS9
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
                                                                                                    TISSUE-COLON;
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                NCBI_TaxID-10090
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003006; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                                                                                            214 AA;
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                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                       25781 MW;
                                                                                                                                                                                                                                                                                                                                                                                                           23922 MW;
69
                                                                                                                                                                                                                                                                                                                                                                    66.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LG_MHC
 . 28
                                                                                                                                                                                                                                                                                                                                                           18;
Score 379.5; DB 1
Pred. No. 9.2e-35;
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Ol-DEC-2001 (TIEMBLEEL. 19, Created)
Ol-DEC-2001 (TIEMBLEEL 19, Last sequence update)
Ol-DEC-2001 (TIEMBLEEL 19, Last annotation updat
HYPOTHETICAL 25.8 MbA PROTEIN (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                     Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL: BC013496; AAH13496.1; -
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; k
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF152371; ADA00242.1;
HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine bilster rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (serv).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ol-MAY-2000 (TERRIFE), 13, Created)
Ol-MAY-2000 (TERRIFE), 13, Last sequence update)
Ol-DEC-2001 (TERRIFE), 19, Last annotation update)
KAPPA LIGHT CHAIN OF MAB7 (FRACMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPFTFGSGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIOLTOSPSSMYASLGERVTITCKASODINSYLSWFOOKPGKSPKTLIYRANRLVDGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 384.5; DB 1
Pred. No. 2.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52BA205FDE995E2A CRC64;
                                                                                              B1C184DA149A16EB CRC64
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DB 11; Length 233;
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Q9JL84
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Best Local
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streptococcal polysaccharide, N-acetyl-glucosamine,
with cardiac myosin.";
Infect. Immun. 68:5803-5808(2000);
                                           MEDILIBE 2014 19942: FUNDEUT-VALLEY, Diamond B.;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant epitope of
"T-Cell-dependent antibody response to the dominant epitope of
                                                                                                                                                                                                                                                                                     01-OCT-2000 (Tremblrel. 15, 01-OCT-2000 (Tremblrel. 15, 01-DEC-2001 (Tremblrel. 19, ANTI-MYOSIN IMMUNOGLOBULIN I
                                                                                                                                                                                                                                                                                                                                                   Q9JL84;
01-OCT-2000
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Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
"The tropism of organ involvement in primary systemic amyloidosis;
contributions of Ig V(L) germ line gene use and clonal plasma cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TIEMBLIER!, 19, Created)
01-DEC-2001 (TIEMBLIER!, 19, Last sequence update)
01-DEC-2001 (TIEMBLIER!, 19, Last annotation update)
KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                           Q9JL84
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                                                                                                      MEDLINE-20448942; PubMed-10992488;
                                                                                                                         STRAIN-BALB/C
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                     (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESGSGSGRDYTETISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESGGGSATNETVTISSLQPEDFATYYCQQYHHLPFTFGPGTKVDFK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIQMTQSPSSLSASVGDRVTFICQASQDIANHLNWYQKKPGEAPKFLIYDGSFLKTGVPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 AA;
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                                                                                                                                                                                                                               Chordata;
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, Last annotation update)
LIGHT CHAIN VARIABLE REGION
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Pred. No. 1.5e-33;
                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
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        RESULT OPEN ACCORD
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Q91WF8
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Best Local Similarity
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Best Local
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091WFB;

01-DEC-2001 (TremBLrel 19, Cru

01-DEC-2001 (TremBLrel 19, Lar

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HYPOTHETICAL 25.9 KDA PROTEIN.
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SMART; SM00406; IGv; 1.
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Interpro; IPR003596; Ig_v.
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                                                                      Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                  Q920E6
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                                NCBI_TaxID=10090;
                                                   Mammalia; Eutheria; Rodentia;
                                                                                                              (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107
107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 AA; 25929 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11648 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.5%;
                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
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093086; 001-DEC-2001 (TIEMBLIFEL. 19, Created)
01-DEC-2001 (TIEMBLIFEL. 19, Last sequence update)
01-DEC-2001 (TIEMBLIFEL. 19, Last annotation update)
PIERIN-MIMICKING ANTI-IDIOTOPE KAPPA CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC015292; AAH15292.1; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                 21 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLYLGVPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSTSSLSASLGDRVXXXCSASQGISNXXXWFQQKPDGTVKLLIYYTSSLXSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                                                                                                                                                                                                                                                    RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTPPFTFGSGTKLEVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 355.5; DB :
Pred. No. 4.7e-32
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Pred. No. 3e-33;
Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACF9B1253ACA1E5D CRC64;
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   Muridae; Murinae; Mus
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Best Local
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O9UL83 PRELIMINARY; PRT;
O9UL83;
O1-MAY-2000 (TrEMBLrel, 13, Created)
                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                             Pfam; PF00047; 1g; 2.
SMART; SM00406; IGV; 2.
                                                                                                                                                                                                                                                                                                                    HSSP; P01607; 1REI.
InterPro; IPR003006; Ig_MH
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                recognizing a cell polarity by using a phage display subtraction
                                                                                                                                                                                                                                                                                                                                                                                                             Shinobara N., Demura T., Fukuda H.:
"Isolation of a vascular cell wall-specific monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BALB/C; TISSUE-SPLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                             233 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLEIK 279
                                                                                                                                               173 DIELTOSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGVPS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20183931; PubMed-10706631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9QYF0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *Definition of the idiotope of Pterin-Mimicking Antibodies Expressed in Mammallan Cells.":
                                                                                                                       61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKVETK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                           1 DIOMTOSPSSISASVCDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPWTFGGGTKLEIX 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RPSGSGSGRDYTFTISSLOPEDIATYYCLQY-DNLWTFGQCTKVEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIOMTOSPSSISASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIQMTQSPASLSASYGETYTITCRASGNIHNYLAWYQQKQGKSPQLLYYNAKTLADGVPS 60
                                                                                                                                                                                                                                                                                                                                                           AB036341; BAA88633.1;
                                                                                                                                                                                                                                                                                                                                                                          Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
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                                                                                                                                                                                                                                                                                  298 AA;
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AA; 11943 MW; DAD3F98E05DD1501 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                   ; ÎGV; Z.
AA; 31867 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                        60.1%;
58.9%;
                                                                                                                                                                                                                                                                                                                                    OHM_B1
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61.7%;
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                                                                                                                                                                                                                      Score 337.5; DB 11; Length 298; Pred. No. 6.6e-30;
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Pred. No. 3.2e-32;
                                                                                                                                                                                                                                                                            E0F96BBA17004317 CRC64;
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                             108 AA
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01-MAY-2000 (TrEMBLrel 13,
01-DEC-2001 (TrEMBLrel 19,
          SEQUENCE
                                                                               Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                       Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (Tremburel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9UL85;
                                                                                                                                    InterPro; IPR003596;
                                                                                                                                                              InterPro; IPR003006; Ig_MHC
                                                                                                                                                                                                                                                                                        "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                            Young D.C
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FRAGMENT)
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Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
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01-DEC-2001 (TERHELFE). 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LICHT CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P80362; 1WTL
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                          P80362;
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FB1E43E7C7AFACCC CRC64;
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Query Match

59.18;

Score 332;

DB 4;

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Result
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230.047 Million cell updates/sec
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd
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                                                       AAW22419
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AAY29916
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AAW22412
AAR60627
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               Human VLA-4 reshap
Alpha-4 integrin m
Human MCP-3 and mu
Human IP-10 and mu
Artificial synthet
                                                                                                                                                                                                                                      Description
                                                                                                                    Mouse anti-VLA-4 a
Mouse VLA-4 antibo
  ME1-14 light chain
                                                                                                                                                            Humanised alpha-4
                                                                                                                                                                               Humanised
                                                                                                                                                                                                 Humanized anti-VLA
                                                                                                                                                                            alpha-4
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Single chain Fv pr	AAY55075	21	260	79.1	5.
rleukin-6	AAY 55072	21	256	79.1	5
RVh-PM1a.	AAR29013	نعا	126	79.1	,
puc-RV1-PMla. Syn	AAR29015	13	126	79.1	S
Human consensus	AAY82345	21	108	79.1	5
Human consensus	AAW70622	19	108	79.1	.5
Human variable lig	AAB61585	22	107	79.1	5
Consensus human 11	AAB60400	22	107	79.1	5
Human V1 consensus	AAB62087	22	107	79.1	5
Humanised anti-alp	AAW87455	20	107	79.1	ū
	AAW70623	19	107	79.3	5
-	AAW86804	19	107	79.3	٠,
Protein encoded	AAW70703	19	237	79.4	5
	AAW10233	18	234	79.4	5
Anti-VEGF humanise	AAW70673	19	110		5
CDR-grafted light	AAW10231	18	108		5
Humanised murine a	AAW70625	19	107	80.0	Ģ
Variable Light dom	AAW86805	19	107		Ġ
R. pipiens recombi	AAW35133	18	355		51
Human/murine 1L-1	AAR47207	15	129	80.3	
Human REI monoclon	AAR65163	16	108		5
noten	AAR26981	13	241		52
Murine OKT4A light	AAR13658	12	109	80.6	<u>5</u>
ed alp	AAW22422	18	107	80.7	5
	AAR81322	16	107		\$
Anti-gp54 MAb T16	AAW26800	19	245	81.0	Ş
d sec	AAY21882	20	241	81.0	55
ScFv(FWP51). Synt	AAR85495	16	240	81.0	55
σ	AAW26797	19	109	81.1	56
ч	AAR26983	13	637	81.9	60
reg	AAR06252	11	128	81.9	Ġ
Murine monoclonal	AAR93159	17	108	82.7	65
Light chain varia	68	16	107	83.9	'n
CD4-specific CDR-	AAR13050	12	234	84.6	5

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ALIGNMENTS

무 ?	PI	×	PΑ	×	PR	X	ΡF	×	PD	×	PZ	×	SO	SO	×	X	×Σ	×	DE	X	7	×	A.	×	Ħ	RESULT AAR81321	
WPI; 1995-269276/35.	Bendig MM, Jones TS, Leger OJ, Saldanha J;		(ATHE-) ATHENA NEUROSCIENCES INC.		25-JAN-1994; 94US-0186269.		25-JAN-1995; 95WO-US01219.		27-JUL-1995.		W09519790-A1.		Chimeric Homo sapiens.	Chimeric Mus musculus.		antibody engineering.	Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;		Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.		02-APR-1996 (first entry)		AAR81321;		AAR81321 standard; Protein; 106 AA.	AT 1	

XPPPX

inflammatory disease.

New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wariable region is directed against leakocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 to Land VII (AM09989) and M099892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5 and 3 construction of a humanized antibody against VLA-4. The 5 and 3 constanting human kappa or gamma-1 constant regions. In the humanized AM099995-99 and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized Light chain, amino acids L45, L49, L58 and L69 in the humanized Clipht chain, amino acids L45, L49, L58 and L69 in the humanized Clipht chain, amino acids L45, L49, L58 and L69 in the humanized Clipht chain amino acid present in the equivalent constitution of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric cantibodies are transfected into COS cells. The humanized antibodies can cell and for treating inflammatory diseases such as multiple cell and for treating inflammatory diseases such as multiple cells of cerebral tranmas, meningits or encephalitis. The antibodies can can be used for detecting VLA-4, for affinity purification or for cenerating anti-inflamens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
Misc-difference 49
                                                                          Misc-difference
                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                      asthma: atheroscierosis: AIDS; dementia, diabetes; tumor, metastasis; inflammatory bowel disease; remential arthritis; transplant rejection; graft versus most disease; nephritis;
                                                                                                                                 Reg 1 or
                                                                                                                                                                                        Region
                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                     Chimeric
                                                                                                                                                                                                                                                                                                                    Chimeric
                                                                                                                                                                                                                                                                                                                                        Chimeric Mus musculus;
                                                                                                                                                                                                                                                                                                                                                                      acute leukocyte mediated lung injury; therapy
                                                                                                                                                                                                                                                                                                                                                                                          atopic dermatitis; psoriasis; myocardial ischaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised alpha-4 integrin antibody 21.6 VL La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW22412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW22412 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence encodes the humanized mouse antibody 21.6 light chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 rfsgsgsgrdytftisslqpediatyyclqydnlwtfgqgtkveik 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 diqmtqspsslsasvgdrvtitcktsqdinkymawyqqtpgkaprllihytsalqpgips 60
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                                                                                                                                                                                                                                                                                                   synthetic
                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                        /note=
                                                                                                                                 /note=
35..49
                                                                                                                                                                                     /note-
24..34
                                /note= "REI Lys-45 is substd. by Lys of mouse 21.6 VL, important in supporting the
                                                                                                                                                /label- CDR1
/note- "21.6
                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                /label= FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                       "REI framework region 2"
                                                                                                                                                                                                       "REI framework region 1'
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                 Toop.
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                                                                                                                                             complementarity determining region 1"
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Pred. No. 1e-36;
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of appropriate fragments of mouse and human DNA sequences. The humanised 21.6 VL and a humanised 21.6 VL (see AAV22413) can be used to produce a claimed humanised 21.6 antibody that is useful in the camentacture of a medicament for treating asthma, atherosclerosis, 20 AIDS, dementia, diabetes, inclammatory bowel disease, rhemmatod at arthritis, transplant rejection, graft versus host disease, unwour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha 4 integrin to use as vaccine or an immunogen. It is also useful for cor generating idiotypic antibodies. The humanised antibody has a confine the human circulation essentially equivalent to that the first in the human circulation essentially equivalent to that the confine the human circulation essentially equivalent to that the confine the human circulation essentially equivalent to that the confine the human circulation essentially equivalent to that the confine the human circulation essentially equivalent to that the confine the human circulation essentially equivalent to that the confine the human circulation essentially equivalent to the confine the human circulation essentially equivalent to the confine the human circulation essentially equivalent to the confine the human circulation essentially equivalent to the confine the human circulation essentially equivalent to the confine the human circulation essentially equivalent to the confine the human circulation essentially equivalent to the confine the humanise essentially equivalent to the confine the human circulation essentially equivalent to the confine the humanise essentially equivalent to that the confine the humanise essentially equivalent to the confine the humanise essentially equivalent to the confine the humanise essentially equivalent to the confine the humanise essentially equivalent to the confine the humanise essentially equivalent essentially equivalent essentiall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide, designated La, comprises the light chain variable region (VI) of a humanised alpha-d integrin antibody 21.6. It is composed of complementarity determining regions (CDRs) from the VL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.6 and a modified human REI framework. It can be expressed in mammalian host cells following PCR amplification and mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; Fig 6; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Uses of humanised alpha-4 integrin antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody
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21.6 VL, located at the binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
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/note= "VL version La (Claim 25)"
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                                                                                                                                                                                                                                                                                             /note- "REI framework region 3"
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                                                                                                                                                                                                                                                                                                                                                                                             02-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                AAR81328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                manufacture of a medicament for treating asthma, atheroscierosis, AIDS, dementia, diabetes, inflammatory bowel disease, rhumatoid arthritis, transplant rejection, graft versus host disease, tumour metastasis, mephritis, atopic dermatitis, psorlasis, mycardial ischaemia, and acute leukocyte mediated lung injury. The humanise antibody has a half-life in the human circulation essentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This polypeptide, designated La, comprises the light chain variable region (VL) of a humanised alpha-4 integrin antibody 21.6 (see also NAM22412). It is composed of complementarity determining regions from the VL region (See AAW2409) of momentarity determining colonal antibody 21.6 and a modified human REI framework. It can be
                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                         antibody engineering.
                                                                                                                                                                                                                                                                                                                                                         Mouse anti-VLA-4 antibody 21.6 light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR81328 standard; Protein; 106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed in mammalian host cells following PCR amplification and mutagenesis of appropriate mouse and human DNA sequences. The humanised 21.6 VL and a humanised 21.6 VL and a humanised 21.6 VL see AMP2411) can be used to produce a claimed humanised 21.6 antibody that is useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Fig 10; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Uses of humanised alpha-4 integrin antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma, atherosclerosis, AIDS, dementia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 rfsgsgsgrdytftissiqpediatyyclqydnlwtfgqgtkveik 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 digmtqspsslsasvgdrvtitcktsqdinkymawyqqtpgkaprllihytsalqpgips 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones ST,
                  50..56
/label- CDR2
                                                /note-
                                                                  /label- FR2
                                                                                    35..49
                                                                                                                                                                                  /note= "mouse light chain variable framework
                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                    /note-
                                                                                                                                    /label- CDR1
                                                                                                                                                                                                      /label- FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                             "mouse light chain variable framework region 2"
                                                                                                "mouse light chain variable
determining region 1"
                                                                                                                                                                  region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 562; DB 18;
Pred. No. 1.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for treatment of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                             complementarity
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RESULT
AAR81326
ID AAR8
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain variable region (without signal sequence). Cloned cDNA CDR sequences of mouse 21.6 variable light and variable heavy regions are linked to human constant framework regions of the REI antibody for the light chain and the 2*CL antibody for the heavy chân in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse CDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L59 in the human kappa LCWR framework are replaced by the anino acid present in the equivalent position of the mouse 21.6 ig light chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context of the context
    AAR81326 standard; Protein; 126 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VIA-4, for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 66; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-269276/35
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                                                                                                                                                                                                61 RESGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                          diqmtqspsslsaslggkvtitcktsqdinkymawyqhkpgkrprllihytsalqpgips
                                                                                                                                                                                                                                                                                                                                                          DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                              rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik 106
                                                                                                                                                                                                                                                                                                                                                                                                                           94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 AA;
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    region 4"
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determining region 2"
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Pred. No. 1
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The sequence represents the mouse antibody 21.6 light chain variable cregion directed against leukocyte adhesion molecule VIA-4. Cloned CC Linke sequences of mouse 21.6 VL and VI (see ANQ9892) regions are callibed against VIA-4. The 5' and 3' ends of the mouse clNAs are constant regions in the construction of a humanized cantibody against VIA-4. The 5' and 3' ends of the mouse clNAs are constant regions. In the humanized light chain, amino acids LA5. C constant regions. In the humanized light chain, amino acids LA5. C constant regions. In the humanized light chain, amino acids LA5. C constant regions. In the humanized light chain, amino acids LA5. C constant regions. In the humanized light chain, ento acids LA5. C constant regions. The humanized light chain, ento acids LA5. C constant regions to the humanized light chain, ento acids LA5. C constant regions to the humanized light chain. Per accordance to the first chain, amino acid present in the equivalent position of the mouse c transfected into COS cells. The humanized antibodies can be used c to transfected into COS cells. The humanized antibodies can be used con also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for meningitis or encephalitis. The antibodies can also be used for meningitis or encephalitis. The antibodies can also be used for the treatment of the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remarks and the constant remark
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detecting VLA-4, for affinity purification or for generating
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The sequence represents the human reshaped antibody 2.6 (19ht chain variable region against leukocyte adhesion molecule VIA-4. Cloned cDNA sequences of mouse 21.6 VI (AAQ99889) and VH (AAQ99892) regions are linked to human constant regions in the construction regions are linked to human constant regions in the construction of a humanized antibody against VIA-4. The 5 and 3 rends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and
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                                                                                                                                                                                                    New humanised antibodies against VLA-4 · used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                           Bendig MM, Jones TS,
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                                                                                                                                               Disclosure; Fig 10; 105pp; English.
                                                                                                                                                                                   inflammatory disease.
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pred. No. 1.8e-32;
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                                                    /note- "framework region 4"
                                                                       /label- FR4
                                                                                                                                  /label= CDR3
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                                                                                                                                                                        /note-
                                                                                                                                                                                              /label- FR3
                                                                                                                                                                                                                                                         /label- CDR2
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                                                                                                                                                                                                                                                                                                                                                                             /label- CDR1
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                                                                                                              "complementarity determining region 3"
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pred. No. 1.8e-32;
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AAY29913
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16-SEP-1999
                                                                                            W09946392-A1
                                                                                                                                                                                         synthetic.
                                                                                                                                                                                                                                                                                                                                                                Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human MCP-3 and murine scFv38 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY29913 standard; Protein; 359 AA
                                                                                                                                                                                                                                                                                                                                                    immune response; HIV; infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 18; Page 68; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma, atherosclerosis, AIDS, dementia, etc.
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Pred. No. 1.8e-32;
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CE The present invention describes fusion proteins comprising a chemokine CC and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise. (1) human monocyte chemokactic protein 3 (MCP-3) and human CC (2) human interferon induced protein 10 (MP-10) and human MCC-1; (3) human macrophage derived chemokine (MDC) and human MCC-1; (4) human SDP-1 and HIV gp120; (7) human MCC-11; (1) human IP-10 and HIV gp120; (6) human MCP-3 and FIV gp120; (7) human MCC-11; (1) human IP-10 and HIV gp120; (7) human MCP-3 and HIV gp120; and (8) human SDP-1 and HIV gp120; (7) human MCP-3 and molecular and sequences encoding them, can be used for producing an immune response, e.g., an effector T cell immune response. They can also be used for treating cancer or treating or response. They can also be used for treating cancer or treating or response. They can also be used for treating cancer or treating or response. They can also be used for treating cancer or treating or consistent of the sequences of the used in in vitro diagnostic assays, as well as in screening assays can the sequence of the constraint of the mapping of the present sequence in the protein antigen epilopes. The present sequence represents a fusion protein
       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 118-119; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
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359 AA;
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AAY29911
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  12-MAR-1998;
                                   12-MAR-1999;
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                                                                                                                                                                                                                                                      Human IP-10 and murine scFv38 fusion protein.
                                                                                                                                          Synthetic.
                                                                                                                                                                                                       immune response; HIV; infection
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98US-0077745
                                   99WO-US05345
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Pred. No. 1.7e-30;
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WPT; 1999-551418/46
                                           Kwak LW,
                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                                                                                                                                                                                                                                                                    Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                               Artificial synthetic construct protein SEQ ID NO:15
                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and a timout antigen or HIV antigen. Specifically claimed fitsol proteins comprise: (1) human monocyte chemotractic protein 3 (MPP-3) and human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-3; (3) human macrophage-derived chemotine (MDC) and human Muc-1; (4) human MCP-3 and HIV gp120; (6) human MCP-3 and HIV gp120; (7) human MCP-3 and HIV gp120; (7) human MCP-3 and HIV gp120; (6) human SP-1; and HIV gp120; (7) human MCP-3 and HIV gp120; (7) human MCP-3 and HIV gp120; (7) human MCP-3 and HIV gp120; and (8) human SP-1; and HIV gp120; The fixton proteins and nuclectide sequences encoding them, can response. They can also be used for treating cancer or treating or revening HIV infection. The fixton proteins and/or nucleotide sequences can be used in In vitro diagnostic assays, as well as in screening assays for identifying unknown tumour antigen epitopes and inc mapping of tumour antigen epitopes. The present sequence represents a fusion protein
                                                                                                                                                                                                                                                                                                                                          immune response; HIV; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY29916 standard; Protein; 374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 rfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 diqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqpgips 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes fusion proteins comprising a chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 115-116; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV antigen, used for treating cancers or treating or preventing HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New fusion polypeptides comprising a chemokine and a tumour antigen or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-551418/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGRDYTFTISSLQPEDIATVYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                      Biragyn A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biragyn A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                          98US-0077745.
                                                                                                                                                                   99WO-US05345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 488; DB 20; Length 361; Pred. No. 1.7e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
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밁 Ş В

Sequence

374 AA;

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HIV 9p120. The fusion proteins, and nucleotide sequences encoding them, can be used for producing an immune response, e.g. an effector T cell immune response. They can also be used for treating cancer on treating or preventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in screening assays for identifying unknown tumour antigen epitopes and fine mapping of tumour antigen epitopes. ANY3916 and ANZ21156 to ANZ21168 are sequences given in the SEO 10 LISTING in the present invention but which are not mentioned further within the specification.
                                                                                                                                                                                                                                                                      Muc-1: (3) human macrophage-derived chemokine (MDC) and human Muc-1: (4) human SDP-1 and human flucti: (5) human in Flore and human flucti: (5) human in Flore and HIV spl20; (6) human SDP-1 and HIV spl20; (7) human MDC and HIV spl20; and (8) human SDP-1 and
                                                                                                                                                                                                                                                                                                                                                         and a tumour antigen or HIV antigen. Specifically chained fusion proteins comprise: (1) human moroyte chemotactic protein 3 (MCP-3) and human Muc-1; (2) human interferon induced protein 0 (IP-10) and human.
                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes fusion proteins comprising a chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 117-118; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
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AAR60627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                             Bigner DD, Carrel S,
N-PSDB; AAQ73537
             WPI; 1994-316669/39
                                                                                                                                               19-MAR-1993;
                                                                                                                                                                               14-MAR-1994;
                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                     04-JUN-1995
                                                                             (ZALU/) ZALUTSKY M R
                                                                                                               (BIGN/) BIGNER D D.
                                                                                                                                                                                                                 29-SEP-1994.
                                                                                                                                                                                                                                                 W09421294-A
                                                                                                                                                                                                                                                                                                            Monoclonal antibody; tumour
                                                                                                                                                                                                                                                                                                                                            ME1-14 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                        AAR60627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR60627 standard; Protein; 128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RESGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 diqmtqspsslsaslggkvtitckasqdinkylawyqhkpgkgprllihytstlqpgips 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                  CARREL S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                             9305-0033864
                                                                                                                                                                             94WO-US02724.
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                                           Zalutsky MR;

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 488; DB 20; Length 374; Pred. No. 1.7e-30; 9; Mismatches 7; Indels
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Method of treating solid or cystic tumours with antibodies - by administering monoclonal antibody Mel-14, having FC deleted,

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RESULT 1
AAR13050
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of the MEI-14 light chain. The protein is monoclonal antibody which can be administered to treat solid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cystic tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                using injection or deposition in the cyst cavity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR13050 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           variable region; antibody; OKT4A; heavy chain; CD4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD4-specific CDR-grafted light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR13050;
Jolliffe LK,
                                                                                                                                                      21-DEC-1990
                                                                                                                                                                                                                              W09109966-A
                                                                                                                                                                                                                                                                                       Region
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                                    (ORTH ) ORTHO PHARM CORP
                                                                           21-DEC-1990;
                                                                                          21-DEC-1990;
                                                                                                               21-DEC-1989;
                                                                                                                                                                                       11-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGRDYTFTISSLOPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 digmtqspsslsaslggkvtltckasqdinkyiawyqhkpgkgprllmhytstlqpgips 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rfsgsgsgrdysfsisnlepediatyyclgydnlltfgggtkleik 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 AA
Zivin RA,
                                                                             90WO-GB02018
                                                                                             89GB-0028874
90WO-GB02017
                                                                                                                                                      90WO-GB02015
                                                                                                                                                                                                                                                                                                                              /label= CDR 3
117..132
                                                                                                                                                                                                                                                                                                                                                                                                                           /label= CDR 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- CDR 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= framework region 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                   /label- kappa constant domain
                                                                                                                                                                                                                                                                                                         /label= framework region 4
                                                                                                                                                                                                                                                                                                                                                                                     /label+ framework region
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                                                                                                                                                                                                                                                                                                                                                                     116
  Pulito VL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 2.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region
     Adair JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Indels
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     Athwal DS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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            CCC CXX PTT PXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Light chain variable region for monoclonal antibody 23F8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR78970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR78970 standard; Protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         See also AAQ12627-Q12632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-DEC-1995
       Hybridoma antibodies have been produced with the spleen cells of BALB/c mouse that had received multiple injections of mercuric ions reacted with glutathione to produce a mercuric ion coordinate
                                                                                     Claim 23; Page 67-68; 106pp; English
                                                                                                                         neutralising heavy metals
                                                                                                                                              New polypeptide(s) which bind heavy metals, esp. mercury - derived from monoclonal antibodies, used for detecting, removing, adding or
                                                                                                                                                                                                    N-PSDB; AAQ97508.
                                                                                                                                                                                                                                                                Lopez 0,
                                                                                                                                                                                                                                                                                                  (BION-) BIONEBRASKA INC
                                                                                                                                                                                                                                                                                                                                           27-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                               27-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                    03-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09520607-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody; heavy metal; mercury; variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 rfsgsgsgteytftisslqpediatyycqqydnllftfgqgtklqi 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGRDYTFTISSLOPEDIATTYCLQYDN-LWTFGQGTKYEI 105
                                                                                                                                                                                                                            1995-275415/36
                                                                                                                                                                                                                                                             Wagner FW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                              94US-0187407
                                                                                                                                                                                                                                                                                                                                                                                  95WO-US01199
                                                                                                                                                                                                                                                                Wylie DE;
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This is an example of a CDR-grafted light chain of the invention. The constant regions are based on sequences of the knman kappa constant domain, the signal sequence is derived from murine MAD 1872. 3 and the CDR sequences are based on the murine OKT4A light chain CDRs. The recombinant antibody encoded by this sequence has affinity for CD4 similar to that of OKT4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New CD4 specific recombinant - complementarity determining region grafted antibody for treating graft rejection and T cell
1 DIOMTQSPSSLSASVGDRYTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                  84.6%; Score 475.5; DB
84.9%; Pred. No. 1e-29;
                                                                                                                                                                                     DB 12;
                                                                                                                               7;
                                                                                                                                   Indels
                                                                                                                                                                                 Length 234;
                                                                                                                                   1.
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RESULT
AAR93159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC covalent compound which was covalently bound to keyhole limpet CC hemocyanin (Kih). Eight hybridomas (IFIO, A10, ICI), 564, 2368, 205, 2368 and 388) were producing what that were strongly positive compound and also were producing what that were strongly positive compound and also were producing what that were strongly positive against glutathone eliminate gualitations mercuric ions law was isolated from bybridoma cells with compound to the primer strand chan synthesis was catalysed were complementary to the 5 and of the CH1 domain of the heavy the primer was for chan synthesis can be presented by the physidoma of interest, or to the 5 and of the CH1 domain of the strand of the Chappa domain. Some of the primers used for cDMA synthesis of the C shown in A097511-097518. The primers used for cDMA synthesis of the C shown in A097511-097518 in the primer sued for cDMA synthesis of the C the primer of a particular antibody polypepide was also used for PCR amplified without the strand compounction with the complement of the primer. In addition, the VH primer AA097518 compounded to amplify the mah 205 and 556 heavy chains. The sequences of the PCR amplified mucleotides were determined. These are given to A0979198971. The descriptions of the SEO to nos given on pp 44-45 and in the claims are different from the descriptions in the second of the claims are different from the descriptions in the second of the claims are different from the descriptions in the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T cell activation; complementarity determining region; CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody: light chain; kappa; variable region; K20; integrin; CD29; beta 1 subunit; humanisation; Hu-K20; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine monoclonal antibody K20 kappa chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR93159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR93159 standard; Protein; 108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence listings. The descriptions in the sequence listings are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 rfsgsgsgrdysfsisnpepediatyyclgydnsiftfgsgtkleik 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGRDYTFT1SSLQPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l diqmtqspsslsaslgykvtitckasqdinkylawyqhkpgkgprillihytstlqpgips 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIOMTOSPSSLSASVCDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALOPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                /note= "framework region'
89.94
/note= "complementarity determining region"
                                                /label- CDR3
                                                                                                                                    /label- FR3
                                                                                                                                                                            /note "complementarity determining region"
                                                                                                                                                                                                                                /label- CDR2
                                                                                                                                                                                                                                                                                                                /label- FR2
                                                                                                                                                                                                                                                                                                                                                        /note= "complementarity determining region"
                                                                                                                                                                                                                                                                            note- "framework region"
                                                                                                                                                                                                                                                                                                                                                                                                        /label- CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "framework region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- FRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 471.5; DB Pred. No. 1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _DB 16; Length 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
        24-JAN-1990;
                                       01-AUG-1990
                                                                       EP380068-A
                                                                                                                                                      Variable region of murine AHT 107 light chain.
                                                                                                                    Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss.
                                                                                                                                                                                       10-DEC-1990 (first entry)
                                                                                                                                                                                                                                              AAR06252 standard; protein; 128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of the variable region of the kappa light chain from murine monoclonal antibody K20. The antibody recognises the beta I subunit (D29) of Integrins and Inhibits activation and proliferation of peripheral T cells induced by anti-CD3 antibodies, Monoclonal antibody K20 is a preferred target for humanisation; the humanised version may be useful as an other section of the humanisation process, the complementarity determining regions (CDBs) of a human antibody with framework regions 70.95% homologous to those of K20 were replaced by the K20
                                                                                                                                                                                                                         AAR06252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanisation of non-human immunoglobulin variable regions - for prodn. of humanised antibodies, esp. K20, e.g. as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 2A; 39pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT26849
                                                                                                                                                                                                                                                                                                                   61 rfsgsgsgrdysfsisnlepediatyyclgyynlwtfgggtkleik 106
                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-162083/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POUL MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bernard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PROT-) PROTEINE PERFORMANCE SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-1994;
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                                                                                                                                                                                                                                                                                   15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             l diqitqspsslsaslggkvtitckasqdinkylawyqhepgkgprllirytsklesgips 60
                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                    86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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        90EP-0101351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94FR-0010858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.7%; Score 465; DB 17;
81.1%; Pred. No. 3.4e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lefranc MP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Margaritte C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 108;
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Search completed: July 9, 2002, 15:40:36
Job time: 122 sec
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                                                                                                                                                                         Query Match 81.9%; Score 460.5; DB 11; Length 128; Best Local Similarity 76.6%; Pred. No. 8.8e-29; Matches 82; Conservative 18; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-1989;
24-JAN-1989;
                                                                                                                                                                                                                                                                    MAbs comprising mouse CH and CL constant regions whith humbs, variable regions may be used to create mouse/human hybrid MAbs, which have a longer serum half-life. Method can be used to produce abs against interleukin-2 receptor and tumour necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1990-232892/31.
N-PSDB; AAQ05556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR THERAPEU.
                                                                                                                                                                                                                                              Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                                         Disclosure; ; p; English.
                                                                                                                                                                                                                                                                                                                                                                 Expression vectors for producing chimeric monoclonal antibodies - which express human constant region and non-human variable region
                                                                 1 DIQMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89US-0441702.
89US-0301216.
                                                                                                                                                                                      1; Gaps
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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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471.
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562
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ggn2_6/ptodata/2/taa/54_COMB_Pep:*
//gn2_6/ptodata/2/taa/54_COMB_Pep:*
//gn2_6/ptodata/2/taa/64_COMB_Pep:*
//gn2_6/ptodata/2/taa/64_COMB_Pep:*
//gn2_6/ptodata/2/taa/64_COMB_Pep:*
//gn2_6/ptodata/2/taa/64_COMB_Pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/laa/backfiles1.pep:*
US-08-561-521-2
PCT USS5-01219-2
PCT USS5-01219-15
US-08-319-582-4
US-08-319-582-4
US-08-318-36-2
US-08-318-36-2
US-08-318-36-2
US-08-318-36-2
US-08-318-318-16
US-08-318-318-17
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US-08-561-521-5
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               US-08-974-899-3
US-08-137-117D-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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124.897 Million cell updates/sec
                                                                                                                                                                                                                                                                                                            Sequence 7, Appli
Sequence 7, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 15, Appli
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                             Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 3, Appl
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     67
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Appli
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438.5	438.5	440.5	440.5	440.5	440.5	440.5	440.5	440.5	441.5	443.5	443.5	443.5	443.5	443.5	443.5	444.5	444.5
78.0	78.0	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.6	78.9	78.9	78.9	78.9	78.9	78.9	79.1	79.1
109	107	214	214	214	109	109	109	107	107	108	108	107	107	107	107	126	126
2	4	u	w	Ν	G	w	2	N	N	Ν	N	IJ	4	Ν	ν	N	1
US-07-934-373C-47	US-09-254-189-1	PCT-US93-0/832-39	US-08-437-642B-39	US-07-934-373C-39	PCT-US93-07832-3	US-08-437-642B-3	US-07-934-373C-3	US-08-652-558-2	US-08-318-157B-6	US-08-116-247-9	US-08-070-116A-/	PCT-US95-01219-6	US-09-025-203-15	US-08-652-558-34	US-08-561-521-6	US-08-436-717-71	US-08-137-117D-71
Sequence						Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence				Sequence	Sequence
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ALIGNMENTS

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US-08-561-521-7
; MOLECULE TYPE: US-08-561-521-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08561521 Patent No. 5840299
                                                                                                                                         INFORMATION FOR SEQ ID NO: 7:
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APPLICANT: Leger, Olivier J.
APPLICANT: Saidanha, Jose
APPLICANT: Jones, S. Tarran
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                           TELEPHONE: 415-5043
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 25-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                      NAME: Smith, William L. REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/561,521
                                           TOPOLOGY:
                                                              STRANDEDNESS:
                                                                                TYPE:
                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
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Sequence

Best Local Similarity Query Match

100.0%;

Score 562; DB 2; Pred. No. 1.2e-45;

Length 106

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                                                                                                                                                                                                                                                                                   Query Match
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GENERAL INFORMATION:
Application
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FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION
TELEPHONE: 415-543-5600
TELEFAX: 415-543-5043
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PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFIWARE: Fatentin Release #10, Version #1.25
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
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                                                                                                                         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                   61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                               Local Similarity
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CITY: San Francisco
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                                                                                                                                                                                                                                                        100.0%; Score 562; DB 5; Length 106; 100.0%; Pred. No. 1.2e-45;
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    Mismatches

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INFORMATION FOR SEQ ID NO: 5:
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                                           CORRESPONDENCE ADDRESS:
                                                                      TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                    APPLICANT:
                                                                                                                                                       APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier
                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
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TELECOMMUNICATION INFORMATION:
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NAME: Smith, William L.
REGISTRATION NUMBER: 30,
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TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
       STREET:
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                                                                                                                                                                                                                                                                                                     61 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106
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                         ADDRESSEE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/561,521 FILING DATE:
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E: Townsend and Townsend Khourie and Crew
One Market Plaza, Steuart Tower, Suite 2000
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Saldanha, Jose
Jones, S. Tarran
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One Market Plaza, Steuart Tower, Suite 2000
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25-JAN-1994
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RESULT 5
US-08-561-521-2
; Sequence 2, Application US/08561521
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         COMPUTER: 1BM PC COMPALIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: PALENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION MUMBER: US/08/561,521
                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                 APPLICANT: Jones S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
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LENGTH: 106 amino acids
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FILING DATE
                                                                                                  MEDIUM TYPE:
                                                                                                                                                          COUNTRY:
                                                                                                                                                                          STATE:
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STRANDEDNESS: sir
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 25-JAN
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Leger, Olivier J.
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Pred. No. 1.2e-40;
6; Mismatches 6; Indels
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; MOLECULE TYPE: protein
US-08-561-521-2
               INFORMATION FOR SEQ ID NO: 15:
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SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SEQUENCE CHARACTERISTICS:
                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Leger, Olivier J.
APPLICANT: Soldenha, Jose
APPLICANT: JONES, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VIA-4
                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/0
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
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                                       TELEFAX:
                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                               NAME: Smith, William L. REGISTRATION NUMBER: 30,223
                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 25-JA
                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 ^
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                                       415-543-5043
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25-JAN-1994
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TOPOLOGY: linear; MOLECULE TYPE: protein US-08-561-521-15
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                                                                           Matches 94; Conservative
                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF ESQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/18
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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FILING DATE: 25-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                               TYPE:
21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                               Local Similarity
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                                     1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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88.7%;
                                                                                90.4%; Score 508; DB 5; Length 126;
88.7%; Pred. No. 1.5e-40;
ative 6; Mismatches 6; Indels
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                                                                              6; Mismatches
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                                                                                                            US-08-339-582-4
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                                                                           sequence 4, Application US/08339582
Patent No. 5558852
                                                                                                                                                                                                                                                                                                                                          Matches
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                                                          GENERAL
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ADDRESSEE: Townseend and Townseend Khourie and Crew
ADDRESSEE: One Market Plaza, Steuart Tower, Suite 2000
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TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: (1006 / 07210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICANT:
                 APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RESGSGSGRDYTETISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                     81 RFSGSGSGRDYSFNISNLEPEDIATTYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                               1 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                       INFORMATION:
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Saldanha, Jose
Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                          Conservative
  Zalutsky, Michael R.
Carrel, Stefan
                                     Bigner, Darell D.
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25-JAN-1994
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                                                                                                                                                                                                                                                                                                                                                            90.4%; Score 508; DB 5; BB.7%; Pred. No. 1.5e-40;
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                                                                                                                                                                                                                                                                                                                             Sequence 22, Applications of the Patent No. 5972656
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                      APPLICANT: Wyle, Dwane E.
APPLICANT: Wyle, Dwane E.
APPLICANT: Wyle, Dwane E.
APPLICANT: OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
NUMBER OF ENQUENCES: 39
              COMPUTER READABLE FORM:
WEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: SIbley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 54
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 DIQMTQSPSSLSASL3GKVTITCKASQDINKYIAWYQHKPGKGPRLLMHYTSTLQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 19-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                           55402
                                                                                                                                                             Minneapolis
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P.O. Drawer 34009
                                                                                                                            USA
            PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 481; DB 1; Length 128; Pred. No. 4.9e-38;
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US-08-888-366-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5571894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                  APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies
TITLE OF INVENTION: Growth Factor Receptor
                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wels, Winfried S. APPLICANT: Hynes, Nancy E. APPLICANT: Harwerth, Ina-Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 14-MAR-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                  CITY: Hawthorne
STATE: New York
FILING DATE:
                 APPLICATION NUMBER:
                                                                                                                                                                        COUNTRY
                                                                                                                                                                                                            ADDRESSEE: CIBA CALLER CORRECT: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGRDYSFSISNPEPEDIATYYCLQYDNSLFTFGSGTKLEIK 107
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REFERENCE/DOCKET NUMBER: 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/888,366 FILING DATE: 03-JUL-1997 CLASSIFICATION: 435
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REGISTRATION NUMBER: 35,
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Similarity 83.2%;
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                                                                                                                                                                                                                                                                                                                                                             No.
                                                                                                                                                                                                                                                                                                                       Recombinant Antibodies Specific for a
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                 US/08/235,838
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Pred. No. 3.1e-37;
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TELEPHONE: (919)541-8614
                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
OFFICIN NUMBER: US 07/828,832
                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hardman, No. 5
APPLICANT: Zwickl, Markus
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                                                     APPLICATION NUMBER: US 0: FILING DATE: 31-JAN-1992 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wels, Winfried S.
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
FILING DATE: 05-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 31-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                               CITY: Summit
                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                    FILING DATE: 05-FEB-1997
                                      APPLICATION NUMBER:
                                                                                                                                                      FILING DATE:
                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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564 Morris Avenue
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                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Groner, Bernd
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05-FEB-1991
                                                                                                                                                   5 June 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth Factor Receptor 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant Antibodies Specific for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ina-Maria
                                      GB 91-810079.3
                                                                                                                                                                       US/08/465,473B
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Patent No. 5571894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                 TELEFAX: (919)541-8689 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
TELEFAX: (908)522 6955
                                                                REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 4-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 637 amino acid
                                                                                                                                                FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                       FILING DATE: 31-JAN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: US 07/828,832
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Recombinant Antibodies
TITLE OF INVENTION: Growth Factor Receptor
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273
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hes 85; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Pfeiffer, Hesna J. REGISTRATION NUMBER: 22,
                                                      TELEPHONE:
                                                                                                             NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                 FILING DATE: TBA
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/235,838
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                                                      (919)541-8614
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                                                                                                                                                                                                                              31-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.9%; Score 460; DB 2; Length 637; 80.2%; Pred. No. 2.6e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant Antibodies Specific for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
                                                                                                                                                                                      GB 91-810079.3
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                                                                                              4-18518/A/CIP/CONT
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LENGTH:

241 amino acids

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-465-4738-11
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                                       TELEFAX: (998)22 6958
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
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                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
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APPLICANT:
                                                                                                                                                                                                          FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pfelffer, Hesna J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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TITLE OF INVENTION: Recombinant Antibodies
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                    APPLICATION NUMBER: GB 91-810079.3
                                                                                                                                                                                                                                                                                                                                             FILING DATE: 5
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEI 241
                                                                                                                                                                    REGISTRATION NUMBER: 22,640
REFERENCE/DOCKET NUMBER: 4-
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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US-08-602-725-29
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              Matches
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                                        Query Match
                                                                                                                                                                                                                                           TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 29,
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                                                                                                              FRAGMENT TYPE: |
ORIGINAL SOURCE:
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                                                                                                                                                       MOLECULE TYPE:
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                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9
FILING DATE: 21-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PG-DOS/MS-DOS
SOFTMARE: PATEBLIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT:
      Local Similarity 83.0%;
hes 88; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
FILING DATE: 19-AU
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
FILING DATE: 02-FEB
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36663
                                                                                                                                                                                                                                                                                                                                          NAME:
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    8; Mismatches
                      Score 454.5;
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Search completed: July 9, 2002, 15:39:04 Job time: 30 sec

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and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Comp
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ALIGNMENTS

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Ig gamma chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Dete: (6-Jan-1995 sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: $29594
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A: Accession: S29594
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A; Residues: 1-178 <SEY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment) (Species: Mus musculus (house mouse) (C:Species: Mus musculus (house mouse) (C:Date: 07-Sep-1990 | sequence_revision 07-Sep-1990 | stext_change 20-dun-2000 (C:Date: 07-Sep:1990 | sequence_revision 07-Sep-1990 | sext_change 20-dun-2000 (C:Date: 07-Sep:1990 | sequence_revision 07-Sep-1990 | sext_change 20-dun-2000 (C:Date: 07-Sep:1990 | sext_change 20-dun-2000 (C:Date: 07-Sep:19
A; Nolecule type; mRNA
A; Residues; 7-120 <ROCI>
A; Residues; 7-120 <ROCI>
A; Cross-references; ENBL: X01820; NID:q51833; PIDN:CAA25962.1; PID:q1333983
A; Rocie; this sequence was determined from the differentiated gene
A; Note: this sequence was determined from the differentiated gene
B; Rocca-Serra, J; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
J. Immunol. 129, 2554-2558, 1982
                                                                                                                                                                                                                                                                                                                                                     A:Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
hypervariable regions.
A:Reference number: $03471; MUID:84057768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Rocca-Serra, J; Watthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, BBO, 2, 867-872, 1983
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RKKLDS TJ. Tonhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Watl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunogiqbulln heavy chain variable region gene expr
                                                                                                                       Ig heavy chain V-1 region (WIL2) - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: D:3348
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A:Molecule type; mRNA
A:Residues: 1-118 cRIS
A:Cress:references: EMBL:218846; MID:333121; PIDN:CAA79298.1; PID:9939900
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterofetramer; immunoglobulin
F:13-99/Domain: immunoglobulin homology <IMMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A: Title: Human anti-self antibodies with high specificity from phage display libraries. A: Reference number: 836256; MUID:93178448
A:Accession: 836265
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CiAccassion: $36265
R;Griffiths, A.D.; Melmqvist, M.; Marks, J.D.; Bye, J.M.: Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [3] heavy chain v region (clone alpha-MUC1-1) - human (fragment)
C:Species: Homo saplens (man)
C:bate: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
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A;Residues: 1:03 4ROC2>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keyvords: heterotetramer; immunoglobulin
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A:Recession: 807453
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A:Title: Biochemical implications from the variable gene sequences of an anti-cytochr
                             R:MY1Vaganam, S.E.; Paterson, Y.; Kaliser, K.; Bowdish, K.; Getzoff, E.D. J. Mol. Biol. 221, 455-452, 1991
                                                                    Ig heavy chain v region (E8) - mouse (fragment)
c;Specids: Mus musculus (house mouse)
c;Aetae: 22-Nov-1993 #sequence_revision 26-Nay-1995 #text_change 21-Jan-2000
c;Accession: S17386
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
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A;Molecule type: mRNA
A;Residues: 1-142 <LAR>
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Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A:Title: Rapid cloning.of rearranged immunoglobulin genes from human hybridoma cells
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A; Accession: A32483
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C:Species: Homo sapiens (man)
C:Date: 12-Oct-1999 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C:Accession: A32483
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A:Accession: D33548
A:Status: pretiminary nucleic acid sequence not shown; not compared with conceptual A:Residues: 1-123 <KIP>
A:Residues: 1-123 <KIP>
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1g heavy chain v region (G6+ CLL-HEN) - human (fragment)
C:Species: Homo sapisons (man)
C:Duto: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0954
R:Mortin, T.: Duffy, S.F.: Carson, D.A.: Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
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A; Residues: 1-122 <MIL>
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A:Accession: S06823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Mol. Biol. 209, 763-778, 1989
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C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: 806823
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A; Residues: 1-117 < MYL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1 OVOLVOSGAEVKKPGASVKVSCKASGFNIKDTYIH-WVRQAPGQRLEWMGRIDPANGYTK 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.2%; Score 459.5; DB 2
73.4%; Pred. No. 3.2e-34;
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C:Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reyvords: immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-116 < MON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the BMBL Data Library, September 1991
A;Description: Cloning and sequencing of the cDNA coding for the variable regions of A;Reference number: $24287
A;Accession: $24289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig gamma chain V region (JS34/32) - mouse
C;Species: Mus musculus (house mouse)
C:Date: 20-E80-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S24289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Reywords: heterotetramer; immunoglobulin
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A; Residues: 1-132 < M
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A:Accession: PH0954
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114 VSS 116
                                          121 VSS 123
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                                                                              61 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARWAGYY-----FDYWGQGTTLT 113
                                                                                                                            62 PKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-EGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                             1 VQLQESGAELVKPGASVKLSCTASVFNIQDTYMHWVRQRPKQGLEWIGRIDPANGNTHFD 60
                                                                                                                                                                                                                        2 VQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYD 61
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                                                                                                                                                                                                                                                                                      88;
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                                                                                                                                                                                                                                                                                                   69.5%; Score 455; DB 2; Length 116; 71.5%; Pred. No. 7.7e-34;
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RESULT S49220

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A:Cross-references: EMBL:237502: NID:g541778; PIDN:CAA85732.1; PID:g541779
A:Experimental source: strain Halb/c
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Reywords: immunoglobulin
F:J-120/Domain: V region *Status predicted <VRG>
F:J-120/Domain: V region *Status predicted <VRG>
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A; Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing a
A; Reference number: $49220
A; Accession: $49220
A; Accession: $49220
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c;species; Mus muscultus (house mouse)
C;baccies; Mus muscultus (house mouse)
C;bate: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C;baccession: 549220
C;baccession: 549220
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A; Residues: 1-221 <KIP>
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C;Species: Homo Sapiens (man)
C;Date: 27-Jan-1955 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
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S46393
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                                                                                       115 QGTLVTVSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                          61 AQKFQGWVTMTRDTSISTAYMELSRLRSDDTAVYYCARDSAYYYDSSGYYSANYYMDVWG 120
                                                                                                                                                                                                                                                            61 DPKFOGRVTITADTSASTAYMELSSLRSEDTAVYYCAREG--YYGNYGVYA----MDYWG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSS 119
                                                                                                                                                                                                                                                                                                                                                    QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60
           KGTTVTVSS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 70.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.7%; Score 450; DB 2; Length 129; 70.5%; Pred. No. 2.4e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 455; DB 2;
Pred. No. 1.5e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 221;
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Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment) C;Species: Nus muscullus (house mouse) A;Variety; strain BNLB/C C;Date: 26.795.1998 #sequence_revision 26.795.1998 #text_change 21-Jan-2000 C;Accession: S03482; S07453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Rocca-Serra, J.;
EMBO J. 2, 867-872,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-43 <MCC2>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F; 15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: this sequence was determined from the differentiated gene R;Noca-Serra, J; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug J.; Rocca-Serra, J; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug J.; Right Somme, G.; Theze, J.; Foug J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; Theze, J.; Fought Somme, G.; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
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A; Molecule type: mRNA
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115 V 115
                                                                                                                        121 V 121
                                                                                                                                                                                                                                61 DPKFQGKATITIDTSSNTAYLQFSSLTSEDTAVYYCARGTTVGR------DYWGQGTTLT 114
                                                                                                                                                                                                                                                                                                                                                61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVOLQQSGAELVKPGASVKLSCTASGENIKDTYMHWVKQRPEQGLEWIGRIDPAKGNTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OVOLVOSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGORLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 2.6e-33;
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A;Cross-references: EMBL:Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840 C;Superfamily: immunoglobulin V region; immunoglobulin homology F;34-117/Domain: immunoglobulin homology <IMM> R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D. submitted to the EMBL Data Library, October 1994 A;Description: Molecular characterization of natural human anti-Sm autoantibodies C;Date: 01-Feb-1995 *sequence_revision 12-May-1995 *text_change 23-Jul-1999 C; Species: Homo sapiens (man) anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human S49530 A; Molecule type: mRNA A; Residues: 1-135 <MAH> RESULT 13 A; Status: preliminary A; Accession: S49530 A; Reference number: S48797 C; Accession: S49530 Best Local Similarity Conservative 68.3%; 7; Mismatches Score 447.5; DB 2 Pred. No. 4.2e-33; DB 2; 16; Indels 11; Gaps Length 135;

1 QVQLVQSGAEVKKPGASVKVSCKASGFNIXDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

N

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A;Accession: PH0960
A:Status: nucleic acid sequence not shown
A;Mcblccule type: DNA
A;Residues: 1-136 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                               R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for sometic selection of natural autoantibodies
                                                                                                                                                                                                                                                        19 heavy chain v region (G6+ T-L30) - human (fragment)
C:Species: Homo sapitans (man)
C:Date: 17-Apr-1933 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0960
                                                                                                                                                    A:Reference number: PH0952; MUID:92202880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Note: this sequence was determined from the differentiated gene R:Notes and sequence was determined from the differentiated gene A:Rocca-Serra, J.: Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere J.; Immunol. 139, 254-2558, 1992

A:Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 1-43 < ROC2>
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A:Residues: 10-120 <ROC1>
A:Cross-references: EMBL:X07144
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C:Species: Mus musculus (house mouse)
A:Variety; strain BALB/C
C:Date: 26:Feb-1998 *sequence_revision 26:Feb-1998 *text_change 21-Jan-2000
C:Accession: 503484 *S07453
C:Accession: 503484 *S07453
R:Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.: Theze, J.; Fougereau, M. EMBO J. 2, 867-872, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Status: preliminary
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A:Accession: S07453
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A;Accession: S03484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GPKFQGXATITADTSSSAAYLQLSSLTSGDTAVYYCTR----GWFRRDAMDYWGQGTSVT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLYT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 OVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVROAPGOGLEWMGWINPNSGCTNY 79
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F;68-98/Region: framework 3
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                                                                                                                                                                                                                                                                                                                                                                   F:15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: heterotetramer; immunoglobulin F;1-30/Region: framework 1
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                       Query Match
121 YGMDVWGQGTTVTVSS 136
                                                                                                                                                                                             Local 5
                                108 YAMDYWGQGTLVTVSS 123
                                                        61 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGRTRVSVSTLYDSSGYYDFSGY 120
                                                                                           61 DPKFOGRVTITADTSASTAYMELSSLRSEDTAVYYCAR------EGYYGNYGV 107
                                                                                                                         1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60
                                                                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                Score 446.5; DB 2
Pred. No. 5.3e-33;
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Search completed: July 9, 2002, 15:39:38 Job time: 64 sec

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OM protein · protein search, using sw model
July 9, 2002, 15:45:57; Search time 15,81 Seconds (without alignments) 301:234 willion cell updates/sec
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Title: Perfect score:

1 QVQLVQSGAEVKKPGASVKV......NYGVYAMDYWGQGTLVTVSS 123 US-09-010-377-2 655

Scoring table: Gapop 10.0 , Gapext 0.5 BLOSUM62

105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR----EGYYGNYGVYAMDYWGQ 115 Ouery Match 65.3%; Score 427.5; DB 1; Length 147; Best Local Similarity 64.1%; Pred, No. 6.3e-36; Matches 82; Conservative 16; Mismatches 25; Indels 5; Gaps

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ALIGNMENTS

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Eukaryota; Metazoa;
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21-JUL-1986
                                                                      HVO7_MVS1. PRY: 139 AA. PO1751: PO1751: PO1752: STANDARD: PRY: 139 AA. PO1751: PO1752: Created)
21.JUL-1986 (Rel. 01. Created)
21.JUL-1986 (Rel. 01. Last sequence update)
15.JUL-1999 (Rel. 38; Last annotation update)
                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Siekevitz M., Gefter M.L., Brodeur P., Riblet R., Marshak-Rothstein A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=83131846; PubMed=6186498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUI-1986 (Rel. 01, Created)
21-JUI-1986 (Rel. 01, Last sequence update)
15-JUI-1999 (Rel. 38, Last annotation update)
19 heavy chain V region 36-65.
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Kammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                            Ig heavy chain V region B1-8/186-2 precursor Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin V region; Antiarsonate antibody: Hybridoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003006; Ig_MHC
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          NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                      62 PKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVTV 121
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                                                                                                                                                                                                                                                                                                                                                                  63.1%;
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                                                                                                                                                                                                                                                                                                                                                                               Score 409;
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Best Local Similarity
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NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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SMART; SM00406; IGv;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J00529; AAA38170.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-81234548; PubMed=6788376;
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                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                            NAMOH
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MEDLINE-83144028; PubMed=6298778,
                                        NCBI_TaxID=9606;
                                                        Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                    Eukaryota; Metazoa;
                                                                                   Homo sapiens (Human)
                                                                                                                                                                P01743;
                                                                                                                                                                              HV1B_HUMAN
              SEQUENCE FROM N.A
                                                                                                   Ig heavy chain V-I region HG3 precursor.
                                                                                                                                                                                                                                                         137
                                                                                                                                                                                                                                                                                   121 VSS 123
                                                                                                                                                                                                                                                                                                                80 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDYYGS---SYFDYWGQGTTLT 136
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                                                                                                                                                                                                                                                                                                                                            DPKFQGRVTITADISASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                        Chordata; Craniata; Vertebrata; Euteleostomi;
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18; Mismatches
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COMPLEMENTARITY-DETERMINING-1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
InterPro; IPR003006; Ig_MHC InterPro; IPR003596; Ig_v.
                                            PIR; A02028; HVMSG7
                                                            EMBL; J00493; AAA38128.1; -.
                                                                                                 or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                            Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                      Capra J.D.;
                                                                                                                                                                                                                                                                                                                              MEDLINE-82152818: PubMed-6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
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Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rechavi G., Ram D., Glazer L., Zakut R., Givol D.; *Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                         "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J00240; AAA52988.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heavy chain V region 93G7 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVQLVQSGAEVKKPGASVKVSCKASGYTFNSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.8%;
79.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG HEAVY CHAIN V-I REGION HG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
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1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

Query Match Best Local Similarity Matches 77; Conserv

Conservative

60.5%; 78.6%;

Pred Score 396;

No. 6.8e-33

Length 117

Mismatches

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    SEQUENCE
                                                  SIGNAL
                                                                                 Pfam; PF00047; ig; SMART; SM00406; IG;
                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                          This SMISS-PROT entry is copyright. It is produced through a collaboration on between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                              Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q., Ohno H., Fukuhara S., Honjo T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HV1G_HUMAN ST/
P23083;
01-NOV-1991 (Rel.
                   NON_TER
                                                                                                                  InterPro; IPR003596; Ig_v.
                                                                                                                                                   PIR; S00476; HVHU35
                                                                                                                                                              EMBL; X07448; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                  heavy-chain locus.";
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88296408; PubMed=2841108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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SMART; SM00406; TGY; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
                                                               Emmunoglobulin V region; Signal.
                                                                                                                                 InterPro; IPR003006; Ig_MHC
                                                                                                                                                                                                                                                                                                                                                             "Dispersed localization of D segments in the human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSS 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHYYG--GSYDFDYWGQGTPLT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYINY
                                                                                                                                                                                                                                                                                                                              7:1047-1051(1988).
  117
117 AA;
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140
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                                                                                   IGv; 1.
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20, Last sequence update)
38, Last annotation update)
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13009 MW; BE61CE63F8CE97BD CRC64;
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Pred. No. 4.2e-33;
                                IG HEAVY CHAIN V-I REGION V35
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FYIA, HUMAN

AC PO1742-7

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Best Local
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SW00406; IGv; 1.
Immnoglobulin v region.
21-JUL-1986
21-JUL-1986
15-JUL-1999
                                                         HV13_MOUSE
P01757;
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-!- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The covalent structure of a human gamma G-immunoglobulin, VII.
acid sequence of heavy-chain cyanogen bromide fragments Hi-H4.",
Biochemistry 9:3161-3170(1970).
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Waxdal M.J., Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-Bevy chain V-I region EU.
16-000 sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The covalent structure of a human
                                                                                                                                                                                                                    121
                                                                                                                                                                                115 VSS 117
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                                                                                                                                                                                                                                                         61 AQXFQGRVTITADESINTAYMELSSLRSEDTAFYFCA-----GGYGIYSPEEY-NGGLVT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYELOMA PROTEIN HAS ALSO BEEN DETERMINED
                                                                                                                                                                                                                    VSS 123
                                                                                                                                                                                                                                                                                DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                      QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY
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117
117 AA;
  (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 390; DB 1;
Pred. No. 2.7e-32;
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Best Local
       | Immunoglobulin V region. | 98 | DOMAIN | 1 | 98 | DOMAIN | 99 | 104 | DOMAIN | 105 | 118 | DISULFID | 22 | 96 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HV51_MOUSE
P06330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
DISULFID 22 96
                                                                                                                                                                                                  Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schilling J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-80078170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region J558.
Mus musculus (Mouse).
                                                                                                                                         InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                MEDLINE=84182519; PubMed=6201362;
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A26242; MHMSJ5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                       SMART; SM00406;
                                                                                                                       Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region AC38 205.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
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                                                                                                                                                                                   A02040; MHMS38.
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117
117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                     ig; 1.
IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=6765983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13024 MW;
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       V SEGMENT.
D SEGMENT.
J SEGMENT.
BY SIMILARITY.
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Pred. No. 4.3e-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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rearrangements in heavy chain V-region gene segments Nature 283:35-40(1980).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schilling J., Clevinger B., Davie J.M., Hood L.; "Amino acid sequence of homogeneous antibodies to dextran
                                        61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                1 QVOLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                   EVOLOOSGPELVKPGASVKMSCKASGYTFTDYYMKWVKOSHGKSLEWIGDINPNNGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE SEQUENCES OF 10 HYBRIDOMA PROTEINS
                                                                                                                                                                                                                                                                                                                                                 292E2AF4BE447E41 CRC64;
                                                                                                                                                                                                                                                                Length 117
-WYFDVWGAGTTVT
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RESULT 10
HV12_MOUSE
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Best Local
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Best Local Similarity
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HY12 MOUSE STANDARD: PRT: 11/ AA. P01756; P17756; P177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musqulus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy chain constant region domains.*;
blochemistry 21:5415-5424(1992).
11 MISCELLAMEDOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOWA PROTEIN HAS ALSO BEEN DETERMINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A02039; MHMS4E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-83075344; PubMed-6816276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 VSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete amino acid sequence of a mouse mu chain: homology among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 VSS 123
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hes 72; Conserv
115 VSS 117
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                                                       121 VSS 123
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                                                                                                                  61 NOKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARD-----YDWY-FDVWCAGTTVT
                                                                                                                                                                                                                                1 EVOLOOSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHCKSLEWIGDINPNNGGTSY 60
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                                                                                                                                                                         DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12983 MW;
                                                                                                                                                                                                                                                                                                                                                                                  59.38;
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Pred. No. 7.7e-31;
                                                                                                                                                                                                                                                                                                                                                                                  Score 373; DB 1;
Pred. No. 1.4e-30
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 117;
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HV48_MOUSE
                  RESULT 12
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Best Local :
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P01755;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibodies: somatic mutation evident in a gamma 2a variable region. "
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region S43 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J00539; AAA38172.1; -. PIR; A02038; G2MS43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell 24:625-637(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-81234548; PubMed-6788376;
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      N1 VWOD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003006;
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                                                                 135 VSS 137
                                                                                                 121 VSS 123
                                                                                                                                                                                                                                                                      Local Similarity
hes 74; Conserv
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                                                                                                                                   NEHFRSKATLTIDKPSSTAYMOLSSLTSEDSAVYYCARY-RLGRY----FDYWGOGTTLT 134
                                                                                                                                                                  DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                     56.7%;
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Pred. No. 2.3e-30;
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COMPLEMENTARITY-DETERMINING-1.
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HV48_MOUSE

STANDARD;

PRT:

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MEDIINE-84182519; PubMed-6201362;
Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
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SMART; SM00406; igv;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "illegitimate recombination generates a class switch delta in an IgD-secreting plasmacytoma."; Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
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23-0CT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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Pred. No. 4.1e-30;
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Immunoglobulin V region.
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Nucleic Acids Res. 8:4839-4840(1980).
NUCLEIC MISCELLANBOUS: FHIS SECUENCE WAS TR
FROM A MYELOMA THAT SECRETES IGG2B.
                                                                                                                                                                                                                Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the cDNA corresponding to the variable region of immunoglobulin heavy chain MPCll.";
Nucleic Acids Res. 8:3591-3601(1980).
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InterPro; IPR003596; Ig_v.
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 23; Mismatches
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            Score 360; DB 1;
Pred. No. 2.8e-29;
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Pred. No. 9.8e-30;
                                                                                                                                                                                                                                                                                                                Sciurognathi; Muridae; Murinae; Mus
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Job time: 373 sec

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134 VSS 136
                           121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-8222252; PubMed-6806831;
Kinapp M.R., Llu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
                                                                                                                                                                                                                                                                                                 (mmunoglobulin V region; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by two adjacent CH genes.";
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by a cloned B-cell lymphoma: a single copy of the VH gene is shared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota; Metazoa; (
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                             80 NOKEKGKATMTYDKSSSTVHMELARLTSEDSANLYCAR--YYGNY----FDYWGOGTTLT 133
                                                                       61 DPKFQCHVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                               1 OVOLVOSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                         70;
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                                                                                                                                                                           55.0%; Score 360; DB 1; Length 136; 56.9%; Pred. No. 3.2e-29;
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Search completed: July 9, 2002, 15:45:57

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Ouery March 69.8%; Score 457.5; DB 4: Length 124; Best Local Similarity 69.5%; Pred: No. 3.8e-41; Matches 91; Conservative 9; Mismatches 16; Indels 15

Indels 15; Gaps

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ALIGNMENTS

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ı,	124 AA; 13580 MW; 1BAAACBD96ACD2A2	NON_TER 124			Pfam; PF00047; ig; 1.	InterPro; IPR003596;	InterPro; IPR003006;	HSSP; P01772; 2FB4.	EMBL; AF035022;	Clin. Immunol.				Wu X., Liu B., Van der Merwe P.L.,	•	·		NCBI_TaxID=9606;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;		(FRAGMENT).	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE		01-MAY-2000 (TrEMBLrel. 13,	01-MAY-2000 (TrEMBLrel, 13,	Q9UL92;	PRELIMINARY; PRT; 124	RESULT 1 Q9UL92	

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                                 EMBL; BC0038...
HSSP; P01842: 7FAB.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
THERPOSS99; Ig.Like.
TRR003500: Ig.Like.
TRR003600: Ig.MHC.
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01-DEC-2001 (TERMILE1. 19, Created)
01-DEC-2001 (TERMILE1. 19, Last sequence update)
01-DEC-2001 (TERMILE1. 19, Last annotation update)
PUTATIVE MATRIX CELL ADHESION MOLECULE-3.
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Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q96QS0
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01-JUN-2001 (TERMELTE1: 17, Created)
01-JUN-2001 (TERMELTE1: 17, Last sequence update)
01-DEC-2001 (TERMELTE1: 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE:
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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                             Interpro: IPR003600; Ig_L:
Interpro: IPR003006; Ig_M
Interpro: IPR003596; Ig_V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 MDYWGQGTLVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE------GYYGNYGVYA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAM-------DY 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMNWVRQAPGQGPEWMGVINPSGGSARY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDVWGQGTTVTVSS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOKFOGRLIMIRDISTSTVYMDLSSLRSDDTAVYFCAREMEITFGGAVSKGFY----YYG 135
        PF00047; 1g; 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.3%; Score 440.5; DB 4 64.9%; Pred. No. 3.4e-39;
                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Mismatches 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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RESULT Q9UL94 ρy

69 TITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGOGTLVTVSS 123

TITSDTSSNTAYLOLSSLTSEDTAVYYCVRR-----GAVVFDYWGQGTALTVSS 109

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SMART; SM00407; IGC1; 3.
SMART; SM00410; IGC1; 3.
SMART; SM00410; IGC1; 1.
PROSITE: PS00219; IG_MHC; UNKNOWN_1.
SBQUENCE 468 AA: 51661 MW; 96352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TIEMBLIE1. 15, Created)
01-OCT-2000 (TIEMBLIE1. 15, Last sequence update)
01-DCT-2000 (TIEMBLIE1. 15, Last annotation update)
01-DCT-2001 (TIEMBLIE1. 19, Last annotation update)
04-DCT-MYOSIN IMMUNOSLOBULIN HEAVY CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with cardiac myosin.";
Infect. Immun. 68:5803-5808(2000).
EMBL; AF206021; AAF69319.1; -.
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MELLINE-20448942: PubMed-10992488;
MELLINE-20449842: PubMed-10992488;
MELLINE-20498942: PubMed-10992488;
MELLINE-20498942: PubMed-10992488;
MELLINE-20498942: PubMed-10992488;
MELLINE-2049842: PubMed-10992488;
MELLINE-20498488;
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MELLINE-20498888;
MEL
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P01810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               streptococcal polysaccharide, N-acetyl-glucosamine,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FRAGMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DPKFQGRYTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                     Local Similarity
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                                                                   9
1 AELVKPGASVKLSCTASGFNIEDTYMHWVKQRPEQGLEWIGRIDPATGHSKYDPKFQGKA 60
                                                              AEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYDPKFQGRV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                       109 AA;
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                                                                                                                                                                                                                                                                                                           11944 MW;
                                                                                                                                                                         66.0%; Score 432; DB 11; 68.7%; Pred. No. 1.7e-38;
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                                                                                                                                          15; Mismatches
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                                                                                                                                                                                                                                                                                                           DFE615FE6CED4EDE CRC64;
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SOR RACE OCCUPATION
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Best Local
                                                                                Strausberg R.;
Strausberg R.;
Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases
EMBL. BC009551, AAH09851.1;
SEQUENCE 614 AA: 67921 MW; 55EF536E77AA9BBB CRC64;
                                                                                                                                                    TISSUE-PRIMARY B-CELLS FROM TONSILS;
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                      Eukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                              01-DEC-2001 (TREMBLEEL 19, Created)
01-DEC-2001 (TREMBLEEL 19, Last sequence update)
01-DEC-2001 (TREMBLEEL 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:15420).
                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                  NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                          096GA6
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SMART; SM00406; IGv; 1.
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MEDILINE-98277139; PubMed-9614934;
MU X., Liu B., Van der Merwe P.L., Kalls N.N., Berney S.M.,
                                        Match 66.0%; Score 432; DB 4; Length 614; Local Similarity 71.5%; Pred. No. 1.5e-37;
                                                                                                                                                                                                                                                                                                                                                                                        117 VSS 119
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Mammalia; Eutheria; Primatos; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DPKFQGRYTITADTSASTAYMELSSLRSEDTAVYYCAREGYYCNYGVYAMDYWGQGTLVT 120
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                                  Conservative
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                               9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local :
  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
                                                                               Q9UL95;
(FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09GYZZ PRELIMINARY; PRT; 119 AA.
09GYZZ, 09GYZZ,
01*MAR-2001 (TYEMBLITEL: 16, Greated)
01*MAR-2001 (TYEMBLITEL: 16, Last sequence update)
01*DEC-2001 (TYEMBLITEL: 19, Last annotation update)
MONOCIONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schistosoma japonicum.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF82622; AGG01452.1;
                                                                                                                                                                                    117 VSS 119
                                                                                                                                                                                                                    121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003006; Ig_MHC InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Song X.T., Feng 2.O., Guan X.H.;
"Amplification, cloning and sequence analysis of the heavy chain variable region gene of monocional anti-idiotypic antibody NP30 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P01772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6182;
                                                                                                                                                                                                                                           61 NQKFKDRVTMTTDKSFSTAYMDLRSLRSADSAVYYCAR--YTDDH--YCLDYWGQGTTVT 116
                                                                                                                                                                                                                                                                        61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                        1 QVOLVESGAEVRKPGASVRVSCKASGYTFTGYYMNWVRQAPGHGLEWIGYINPSRGYTNY 60
                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 VSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 AOKFODRYTITRDRSMNTAYMELSSLRSEDTAMYYCAR-GYSSSWD-DAFDIWGOGTMYT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DPKFOGRVTITADTSASTAYMELSSLRSEDTAVYYCARBGYYGNVGVVAMDYWGOGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00410; IG_like; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119
119 AA;
                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   119
; 13567 MW; BA893873FD5FA6AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             65.3%; Score 428; DB 5 66.7%; Pred. No. 5e-38;
                                                                                                                                                                                                                                                                                                                                                                             17; Mismatches
                                                                                             PRT;
                                                                                             125 AA
                                                                                                                                                                                                                                                                                                                                                                                                        DB 5; Length 119;
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Best Local
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                                                      Matches
                                                                   Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P01810; 2FBJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003006; Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF035019;
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                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
VH186.2-D-J-C MU PROTEIN (FRAGMENT).
                                                                                                                                                                          Kozono Y., Kozono H., Akuma T.;
Blreet Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitropheny) Abecty (Mp. 7;
Submitted April 2007
                                                                                                                                                                                                                                                 STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                       NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                               Q924Q3
                                                                                                                         SEQUENCE
                                                                                                                                                                   EMBL; AB067797; BAB63282.1; -.
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                       NON_TER
                                                                                                                                                    NONLTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 VTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AQKVQGRVTMTRDTTISTAYMELSRLRSDDTAVYYCARSQGGGRIAAAGDAFDIWGQGTM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 OVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                   Local Similarity
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                        1, QVQLVQSGAEVKKPGASYKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPKFOGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVY--AMDYWGQGTL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D.C
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Liu B., Van der Merwe P.L., Kalis N.N., Berney
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125
                                                                                                                           146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                        146
                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13516 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.8%;
                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                     65.2%;
                                                                                                                           16136 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Mismatches
                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 428; DB 4; Length 125; pred. No. 5.3e-38;
                                                        Score 427; DB 11; Length 146; Pred. No. 8.3e-38; 7; Mismatches 23; Indels
                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OD3CD5C232488EAC CRC64;
                                                                                                                           CEA8DD6E1955807F CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   146 AA
                                                                                                                                                                                                                                                                                                                                                              update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARABAGA T. SHATEGAMA A. SCHOTTINE M., Itch M., Itch M., Ishii Y., Kawai I. Sharaqawa A. Shibata K. Yoshino M., Itch M., Ishii Y., Rawai A. Fikunishi Y., Konno H., Adachi J., Fukuda S., Ra Airawa K., Izawa M. Nishi K. Kiyosawa H., Kondo S., Yamanaka I., Ra Lizawa K., Izawa M. Nishi K. Kiyosawa H., Kondo S., Yamanaka I., Ra Lizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ra Lizawa K., Washawa T., Sahio R., Ra Kadota K., Marisuda H.A., Ashburner M., Batalo S., Casawati T., Ra Kadota K., Marisuda H.A., Ashburner M., Batalo I., Koshiwa H., Ra Helsohman M., Batalo I., Pasche G., Quackenbush J., Ra Felsohman M., Batalo I., Washio T., Ra Kuchi P., Lewis S., Matsuo Y., Nikaio I., Peoche G., Quackenbush J., Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Ra Sakai K., Okido T., Furuno M., Aono arrinci P., de Bonaldo M.F., Ra Sakai K., Okido T., Furuno M., Aono arrinci P., de Bonaldo M.F., Ra Bake J., Boffelli D., Bojinga N., Carrinci P., de Bonaldo M.F., Ra Haroshioni L., Mashima J., Mazaareli J., Momboerts P., Ra Gustincich S., Hall D., Hoffmann M., Hume D. A., Kamya M., Lee N. H., Ra Nordone P., Ring B., Ringwald M., Kodriguez T., Shibata Y., Storch K.-F., Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Ra Sasaki H., Toyo-Oka K., Wang M. H., Weltz C., Wilming L., Ra Myyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Ra Myyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Ra Myyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Ra Myyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                      Matches
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                                                                                                                                                        Best Local Similarity
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01-DEC-2001 (TrEMBLrel.
1810060009RIK PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE-PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 VSS 121
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                                                                                                                                                                                                                                                                                           SMART; SM00406; IGV; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:96443; Igh-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK007918; BAB25349.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
61 DPKFQGRYTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGYYAMDYWGQGTLYT 120
                                          20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTYY 79
                                                                                     1 QVOLVQSGAEVKKPGASVKVSCKASGFNIKDTYTHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P01842;
                                                                                                                                                                                                                                                                                                                                                                                                      ; IPR003599; Ig.cl.
; IPR003597; Ig.cl.
; IPR003600; Ig_like.
; IPR003006; Ig_MHC.
; IPR003596; Ig_v.
                                                                                                                                                                                                                                                   PS00290; IG_MHC; UNKNOWN_1
473 AA; 51699 MW; 9DED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 17,
(TrEMBLrel. 17,
(TrEMBLrel. 19,
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                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7FAB
                                                                                                                                                           64.4%; Score 422; DB 11;
65.9%; Pred. No. 1.2e-36;
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                                                                                                                                            19;
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                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                          9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            473 AA
                                                                                                                                                                                          DB 11;
                                                                                                                                                  19;
                                                                                                                                                                                             Length 473;
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                             *Kozono Y., Kozono H., Azuma T.;
*Direct Estimation of Relative Affinity by Flow Cytometry Reveals.
Affinity Maturation of B Cell Antigen Receptors in Response to (4.

Bydroxy-3-Nitrophenyl)Acetyl (MP).*,

Submitted (AuC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL: AB067789: BAB63274.1: **MEL/GenBank/DDBJ databases.
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0924R1;
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01-DEC-2001 (TERBLIE). 19, Last sequence update)
01-DEC-2001 (TERBLIE, 19, Last annotation update)
VH.B6.2-D-J-C MU PROTEIN (FRAGMENT).
                                                                                                                                                                         STRAIN-C57BL/6;
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Haturation of Relative Affinity Haturation of B Call Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).*;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NEKEKSKATLTVDKPSSTAYMOLSSLTSEDSAVYYCARSDY--DYD-YAMDYWGOGTSVT 117
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Pred. No. 1.4e-36;
17; Mismatches 23; Indels 3;
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Q924R8;
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Q9UL89;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
                    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Witrophenyl)Acetyl (NP).
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
VH186-2-D-J-C MU PROTEIN (FRAGMENT)
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Pred. No. 3.3e-36;
                                                                                                                                  PRT;
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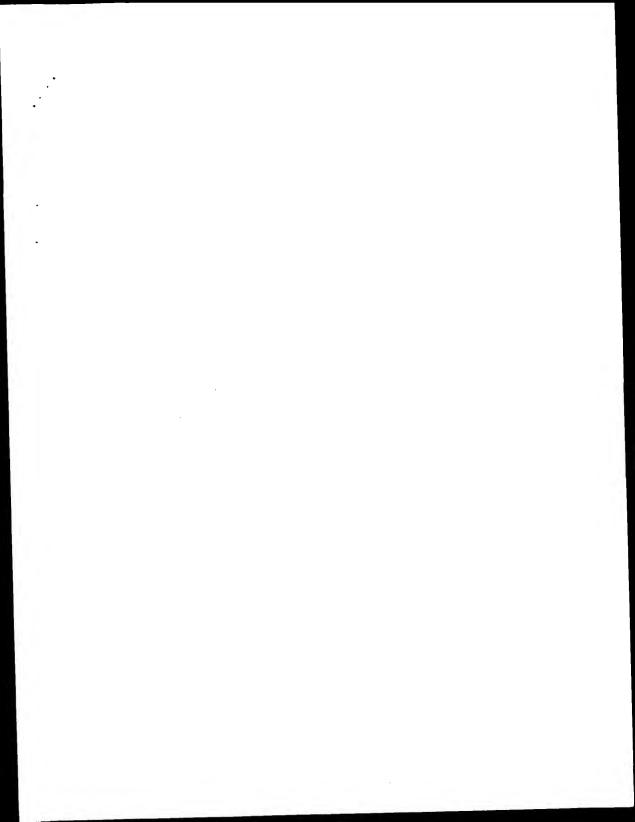
AC 092406

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Best Local Similarity 72.5%; Pred. No. 2.8e-36;
Matches 87; Conservative 3; Mismatches 25
                                                                                                                                                                                                                                                                         Query Match
Best Local
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MEDLINE-9827119; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     092406 PRELIMINARY: PRT; 145 AA. 092406; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) VH186.2-D-J-C MU PROTEIN (FRAGMENT).
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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"Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Hittophenyl)Acetyl (NP).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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hes 79; Conserv
61 NEKEKSKATLTYDKPSSTAYMQLSSLTSEDSAVYYCARSTLSHY-----YAMDYWGQGTS 115
                                                          61. DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE - - GYYGNYGVYAMDYWGQGTL 118
                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFN1KDTY1HWVRQAPGQRLEWMGRIDPANGYTKY 60
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116 AA; 12605 MW; C8F9131DE13EA898 CRC64;
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Maximum DB seq length: 2000000000
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Humanised alpha-4
Mouse anti-VLA-4 a
Mouse VLA-4 antibo
                                             Alpha-4 integrin m
Heavy chain variab
A fusion of single
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Chimaeric human/mu
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AAR81323 standard; Protein; 123

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×	123 AA.
X AC	AAR81323;
XX	02-APR-1996 (first entry)
XX	Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.
XXX	Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic; antibody engineering.
S X	Mus musculus.
ΧP	W09519790-A1.
XX X	27-JUL-1995.
X P Y	25-JAN-1995; 95WO-US01219.
X PR	25-JAN-1994; 94US-0186269.
ΧX	(ATHE-) ATHENA NEUROSCIENCES INC.
XX PI	Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX	WPI; 1995-269276/35.
rd Ld	New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothalial Collagorian
×	inflammatory disease.
PS	Claim 11; Page 69; 105pp; English

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20..49
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132..142
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                                                                                                                                                                                                                                                                                               "complementarity determining region 1"
                                                                                                                                        "framework region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                           "signal peptide"
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Pred. No. 5.5e-53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents the human reshaped antibody 21.6 heavy chain variable region against leukocyte adhesion molecule VLA-4. Cloned cDMA sequences of mouse 21.6 VH (AAQ9982) and VL (AAQ9882) cloned cDMA sequences of mouse 21.6 VH (AAQ9982) and VL (AAQ9882) construction regions are linked to human constant regions in the construction regions are linked to human constant regions in the construction of the farman and 3 construction mouse collars are modified using PCR primers (AAQ9985-88) and then mouse cDMAs are modified using PCR primers (AAQ9985-88) and then subcloned into mammalian cell expression vectors containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing human containing huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New humanised antibodies against VLA-4 - used for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AA099894.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           generating anti-idiotype antibodies.
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asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis;
                                                                 Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
                                                                                                                                       Humanised alpha-4 integrin antibody 21.6 VL version Ha
                                                                                                                                                                                                                  09-DEC-1997 (first entry)
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100.0%; Pred. No. 6.4e-53;
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manufacture of a medicament for treating asthma, atherosclerosis, AIDS, dementia, diabetus, inflammatory bowel disease, risumanoid arthritis, transplant rejection, graft versus bost disease, tumou retastasis, nephritis, atopic dermatitis, psortasis, mycorrdial ischaemia, and acute leukocyte mediated ung injury. The humani antibody has a half-life in the human circulation essentially
                                                                                        This polypeptide, designated Ha, comprises the heavy chain variable region (VH) of a humanised alpha-4 integrin antibody 21.6 (see also ANW22413). It is compased of complementarity determining regions from the VH region (see ANW22410) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human 21/28 CL framework. It can be expressed in mammalian host cells following PCR amplification and mumanised 21.6 VH and a humanised 21.6 VL (see ANW22412) can be used to produce a claimed humanised 21.6 antibody that is useful in the
equivalent to that of naturally occurring human antibodies
                                                                                                                                                                                                                                                             asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                       Uses of humanised alpha-4 integrin antibody . for treatment of
                                                                                                                                                                                                                                       Example 6; Fig 11; 107pp; English.
                                                                                                                                                                                                                                                                                                             N-PSDB; AAT74789
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                                                                                                                                                                                                                                                                                                                                                                           (ATHE-) ATHENA NEUROSCIENCES INC
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WO9718838-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qvqlvqsgaevkkpgasvkvsckasgfnlkdtylhwvrqapgqrlewmgrldpangytky 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
               /note= "21/28'CL framework region 4"
                                 /label- FR4
                                            /label= CDR3
/note= "21.6 complementarity determining region
                                                                                              /note= "21/28'CL Arg-72 is substd. by Ala of mouse 21.6 VL, important in supporting the CDR2
                                                                                                                                                                                                           /note= "21/28'CL framework region 50..66
                                                                                                                                                                       /note= "21.6 complementarity determining region 2" 67..98
                                                                                                                                                                                                                                              /note= "21.6 complementarity determining region 1" 36..49
                                                                                                                                         /note= "21/28'CL framework region
                                                                                                                                                           /label- FR3
                                                                                                                                                                                               /label= CDR2
                                                                                                                                                                                                                                   /label- FR2
                                                                                                                                                                                                                                                                      /label- CDR1
                                                                                                                                                                                                                                                                                                             /note- "21/28'CL residues 27-30 are replaced by
                                                                                                                                                                                                                                                                                                                                          /note= "21/28'CL framework region 1"
                                                                                                                                                                                                                                                                                                                                                           /label- FR1
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                            binding*
                                                                                           door.
                                                                                                                                                                                                                                                                                                   those of MAb 21.6, involved in antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 655; DB 18;
Pred. No. 6.4e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT
AAR81330
ID AAR
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                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                  용
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 manufacture of a medicament for treating astuma, atheroscleros is manufacture of a medicament for treating astuma, atheroscleros is along dementia, diabetes, infiammatory bowel disease, risumatoid arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial schematists, psoriasis, myocardial schematists, pastissis, pastissis, myocardial for schematists, pastissis, pastissis, myocardial for schematists, and caute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin for use, as a vaccine or a immunogen. It is also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This polypeptide, designated Ha, comprises the heavy chain variable region (VH) of a humanised alpha-4 integrin antibody 21.6. It is composed of complementarity determining regions (CDRs) from the VH region (see AAW22410) of mouse alpha-4 integrin monochone antibody region (see AAW22410) of mouse alpha-4 integrin monochone and the separate of 1.6 and a modified human 21/28 CL framework. It can be expressed in mammalian host cells following PCR amplification and mutagenesis of mouse and human DAM sequences. The of appropriate fragments of mouse and human DAM sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Uses of humanised alpha-4 integrin antibody - for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; Fig 7; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for use as a vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibody has a half-life in the human circulation essentially equivalent to that
                                                                                                                     Mouse anti-VLA-4 antibody 21.6 heavy chain variable region.
                                                                                                                                                                 02-APR-1996 (first entry)
                                                                                                                                                                                                        AAR81330;
                                                                                                                                                                                                                                               AAR81330 standard; Protein; 123 AA
                   Mus musculus.
                                                             antibody engineering.
                                                                              Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                    121 vss 123
                                                                                                                                                                                                                                                                                                                                                                                              121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 98.9%;
Local Similarity 99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                               61 dpkfqgrvtitadtsastaymelssirsedtavyycaregyygnygvyandywgqgtlvt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 OVOLVOSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones ST, Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US18807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 648; DB 18; Length 123; Pred. No. 2.4e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yednock TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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PXX
                                      The seguence represents the mouse anti-VLA-4 antibody 21.6 heavy chain crisis of wariable region (without signal sequence). Cloned COMA CDR sequences of CC wariable 13th and variable heavy regions are linked to human CC mouse 21.6 variable 13th and variable heavy regions are linked to human CC constant framework regions of the REI antibody for the light chain and CC constant framework regions of the REI antibody for the light chain and CC constant and the subcloned into CC madmalian cell expression vectors containing human kappa or gamma 1 CC mammalian cell expression vectors containing human kappa or gamma 1 CC constant regions. In the human kappa LCVR framework are replaced by the amino CC colls and L69 in the human kappa LCVR framework are replaced by the amino CC colls. The human kappa LCVR framework are replaced into CCS chain. Plasmids encoding the chimeric antibodies are transfected into CCS cells. The humanized antibodies can be used to inhibit adhesion of a semiliple sclerosis. They can also be used in the treatment of sexess such cerebral traumas, maningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating containing the containing variables.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JUL-1995.
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                                                                                                                                                                                                                                                                                                                   Disclosure; Page 68; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                           New humanised antibodies against VLA-4 - used for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-269276/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bendig MM,
                                                                                                                                                                                                                                                                                                                                                inflammatory disease
                                                                                                                                                                                                                                                                                                                                                              leukocyte adhesion to endothelial cells, partic. for treating
Sequence
                            anti-idiotype antibodies.
    123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-0186269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "mouse heavy chain variable framework
    region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note- "mouse heavy light chain variable framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113..123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "mouse heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "mouse heavy chain variable framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse heavy chain variable framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "mouse heavy chain variable complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "mouse heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                            Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       determining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chain variable complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region
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AAR81327
            The sequence represents the mouse antibody 21.6 heavy chain variable region directed against leukocyte adhesion molecule VIA-4. Cloned CDNA sequences of mouse 21.6 VH and VL (see AAQ99889) regions are
                                                                                          Disclosure; Flg 2; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                      New humanised antibodies against VLA-4 - used for inhibiting loukocyte adhesion to endothelial cells, partic, for treating
                                                                                                                                 inflammatory disease.
                                                                                                                                                                                                          N-PSDB; AAQ99892
                                                                                                                                                                                                                         WPI; 1995-269276/35.
                                                                                                                                                                                                                                                             Bendig MM,
                                                                                                                                                                                                                                                                                           (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                    25-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse VLA-4 antibody 21.6 light heavy variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR81327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR81327 standard; Protein; 140 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 vss 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l evqlqqsgaelvkpgasvklsctasgfnlkdtylhcvkqrpeqglewigridpangytky 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OVOLVOSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGORLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                             94US-0186269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118.,131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "complementarity determining region 1"
55..68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "signal peptide" 20..49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note-
                                                                                                                                                                                                                                                      Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "framework region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.7e-43;
                                                                                                                                                                                                                                                      Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alliked to human constant regions in the construction of a humanized antibody against VLA-4. The 5 and 3 ends of the mouse colks are modified using peck primers (See Anglags-98) and then subcloned into a mammalian cell expression vectors containing human kappa or gammal Constant regions. In the humanized heavy chain, manino acids H27, H28, H29, H30, H44 and H71 in the heavy chain, manino acids H27, by the amino acid present in the equivalent position of the mouse call fight chain. Plasmids encoding the chimeric antibodies are containing that the state of the containing the chimeric antibodies are containing that the chain the containing the chimeric antibodies are containing that the containing the chimeric antibodies are contained to treat inflammatory diseases such as multiple solerosis. They can also be used in the treatment of stroke, cerebral traumans, considered to treat value for affairty metalication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                         Region
                                                                                               Region
                                                                                                                                                  Region
                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                             metastasis; inflammatory bowel disease; rheumatord arthritts; transplant rejection; graft versus host disease; nephritts; atopic dermatitis; psocialsis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                      asthma; atherosclerosis; AIDS; dementia; diabetes; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha-4 integrin mouse MAb 21.6 VH region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW22410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW22410 standard; Protein; 140 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 v 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 V 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 dpkfqgkatitadtssntaylqlssltsedtavyfcaregyygnygvyamdywgqgtsvt 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DPKFOGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 evqlqqsgaelvkpgasvklsctasgfnikdtylhcvkqrpeqglewigridpangytky 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 OVOLVOSGAEVKKPGASVKVSCKASGENIKDTYIHWVROAPGORLEWWGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                           /note-_ "complementarity determining region 2"
/note= "framework region 3"
                     /label- FR3
                                                                         /label- CDR2
                                                                                                           /note
                                                                                                                              /label- FR2
                                                                                                                                                  /note- "complementarity determining region 1"
                                                                                                                                                                               /label- cDR1
                                                                                                                                                                                                             /note= "framework region 1"
                                                                                                                                                                                                                                     /label- FR1
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                       /label- Leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.1%; Score 544; DB 16;
82.6%; Pred. No. 1.1e-42;
ative 11; Mismatches 10;
                                                                                                      "framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody that is used in the manufacture of a medicoment for treating a disease selected from asthma, atherosclerosis, AIDS, treating a disease selected from asthma atherosclerosis, aIDS, dementia diabetes inflammatory bowel disease, rheumatod treating arthritis, transplant rejection, graft versus host disease, tumour metastasis, reportatis, atopic dementitis, psoriasis, mycordial ischaemia, and soute leukocyte mediated lung injury. The antibody ischaemia, and soute leukocyte mediated lung injury at the articular portification of alpha integring may also be used in the affinity purification of alpha integring may also be used in the affinity purification of alpha at integring may also be used in the affinity purification also useful for energia diotypic antibodies. The humanised antibodies of the invention have a half-life in the human circulation essentially invention have a half-life in the human circulation essentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 69-70; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Uses of humanised alpha-4 integrin antibody - for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse anti-alpha-4 integrin monoclonal antibody 21.6. The complementarity determining regions (CDRs) of the 21.6 VH can be incorporated into a human 21/28/CL framework to produce a claimed humanised 21.6 VH (see AAW22413) and a claimed humanised 21.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT74760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                equivalent to that of naturally occurring human antibodies
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Heavy chain variable region of humanised NR-LU-13 antibody NRX451
                                            05-JUN-1998 (first entry)
                                                                                   AAW44124;
                                                                                                                          AAW44124 standard; Protein; 120 AA.
                                                                                                                                                                                                                                 140 v 140
                                                                                                                                                                                                                                                                     121 V 121
                                                                                                                                                                                                                                                                                                            61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                          20 evqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewigridpangytky 79
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 83.1%; Score 544; DB 18; Local Similarity 82.6%; Pred. No. 1.1e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A novel humanised Ab (hAb) binds the antigen bound by NR-IU-13. The hAb, specifically NRX451, or its conjugates can be used for the manufacture of a diagnostic or medicament for cancer diagnosts or treatment. The hAb has reduced immunogenicity and toxicity in humans, but retains the ability to bind the NR-IU-13 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Graves SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the heavy chain variable region of the humanised murine anti-human cancer antigen antibody (Ab) NR-LU-13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 4; 100pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy and immunodiagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised antibody binds same human cancer antigen as antibody NR-LU-13 - useful for pre-targeting methods, conventional antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NEOR-) NEORX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                              02-APR-2001
                                                                     AAB30693;
                                                                                                         AAB30693 standard; Protein; 431 AA
                                                                                                                                                                                                                                                    121 VSS 123
                                                                                                                                                                                                                118 vss 120
                                                                                                                                                                                                                                                                                           61 dlsfqgrvtitadtsintaymelsslrsddtavyycsrevl---tgtwsldywgqgtlvt 117
                                                                                                                                                                                                                                                                                                                                     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                              (first entry)
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82.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 523.5; DB 1
Pred. No. 6.9e-41;
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03-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer, e.g. adenocarcinomes or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and a cloning site for insertion of a second nucleic acid sequence uncoding a polypeptide to be fused with streppayedint. Interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a first nucleic acid operatively linked to a promoter, encoding a polypeptide to be fused with streptaydin, and cloning site for insertion of a second nucleic acid encoding at least cloning site for insertion of a second nucleic acid encoding at least 23 mains acids of streptaydin or its functional variant. The issue of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-091213/10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NEOR-) NEORX CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fusion proteins. The vector comprises a first nucleic acid encoding streptavidin or its functional variant operatively linked to a promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 10; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                               265
                                                                                                       121
                                                                                                                                                                  208
                                                                                                                                                                                                                                                                         148 qvqlvqsgaevkkpgasvkvsckasgfnlkdtymhwvrqapgqglqwmgridpangntks 207
                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                     1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                          dlsfqgrvt1tadtsintaymelsslrsddtavyycsrevl---tgtwsldywgqgtlvt 264
                                               vss 267
                                                                                                           VSS 123
                                                                                                                                                                                                                      DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                        102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e.g. adenocarcinomas -
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Graves SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     990S-0137900
990S-0168976
                                                                                                                                                                                                                                                                                                                                                                                                                                    79.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schultz JE,
                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 523.5; DB 1
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGP40; EPCAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sanderson JA,
                                                                                                                                                                                                                                                                                                                                                                                                            indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                            Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reno JM.
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERSONAL PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                     Matches 103;
                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR76681 standard; Protein; 136 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA094599 encodes AAR76681 the human/murine chimeric antibody HEF-
RVL-M21g(gamma)]. The antibody is reactive with human medulio-
blastoma (a brain tumour) cells. The chimeric antibody can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ94539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohtomo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pept1de
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        medulloblastoma; brain tumour; treatment; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; murine; chimeric antibody; HEF-RVL-M21g(gamma)1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human/murine chimeric antibody HEF-RVL-M21g(gamma)1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 26; Page 94; 120pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reconstituted antibody against human mcdullo:blastoma cells -contains high proportion of human antibody origin and has low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        used in the diagnosis and treatment of this disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antigenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-200347/26
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08
                                                                                                              20
                                                                                                                                                                                                                                                                     Local Similarity
                                                       61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
dpkfqgrvtitadestntaymelss1rsedtafyfca-sayyvn----qdywgqgttvt 133
                                                                                                           qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpadgntky 79
                                                                                                                                                                          QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sato K,
                                                                                                                                                                                                                                                                                                                                                                                        136 AA;
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93JP-0291078
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87..118
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119..126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label- CDR 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= CDR 3
127..136
                                                                                                                                                                                                                                                                 79.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsuchiya M;
                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                 Score 523; DB 16;
Pred. No. 8.8e-41;
                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                             Length 136;
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RESULT
AAW04396
ID AAW
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                                     cultured, and the expression prods. of the heavy and light chain DNA mols. sepd. and connected with a peptide linker to produce a single strended Pv region. The reshaped Pv region has low human antigenicity, and is therefore expected to be useful as an agent for the diagnosis and treatment of cerebral tumours.
                                                                                                        constant region sequences, respectively to produce chimaeric human/murine light and heavy chain DNA mols. A recombinant vector for the expression of the heavy and light chain DNA mols. was prepd., and used to transform a host cell. The host cell was then
                                                                                                                                                            monoclonal antibody (MAb) ONS-MA1. The MAb was prepd by combining light and heavy variable region DNA, from a murine anti-human myeloblastoma cell MAb, with human light and heavy
Sequence
                                                                                                                                                                                                                                                            Reshaped anti-human myeloblastoma cell human antibody - has low human antigenicity, and is therefore useful for diagnosis and treatment of cerebral tumours, e.g. myeloblastoma
                                                                                                                                                                                                      The present sequence is a fragment of the chimaeric human/murine
                                                                                                                                                                                                                                   Example 5; Pages 38-39; 45pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-1994;
19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                      18-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-M21-g(gamma)1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis; treatment; cerebral tumour; reshaped
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine; human; myeloblastoma; chimaera; monoclonal antibody; chimera; single stranded Fy region; low human antigenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-DEC-1996
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                            myeloblastoma
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                                                                                                                                                                                                                                                                                                                           AAT38653
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136 AA
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                                                                                                                                                                                                                                                                                                                                                                                           94JP-0252166
93JP-0291078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= CDR_2
118..125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= CDR_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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Query Match

79.8%;

Score 523;

DB 17;

Length 136;

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XX SO XX
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AAR76682
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Matches 103; Conservative
                                 AAQ94548 is the plasmid pscrvT7-hu21, which encodes AAR7682 the human antibody ONS-401 Fv fragment. The plasmid was used in the construction of an expression vector, conty, cDMA encoding a human/murine chimeric antibody, reactive with human medullohustoma. (a brain tumour) cells. The chimeric antibody can be blastoma. (a brain tumour) cells. The chimeric antibody can be
 Sequence
                                                                                                                                                       Reconstituted antibody against human medullo:blastoma cells contains high proportion of human antibody origin and has in
                       used in the diagnosis and treatment of this disease
                                                                                                                  Claim 35; Pages 98-99; 120pp; Japanese
                                                                                                                                                antigenicity
                                                                                                                                                                                                    N-PSDB; AAQ94548
                                                                                                                                                                                                                WPI; 1995-200347/26
                                                                                                                                                                                                                                           Ohtomo
                                                                                                                                                                                                                                                                                               19-NOV-1993;
                                                                                                                                                                                                                                                                                                                        19-OCT-1994;
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                                                                                                                                                                                                                                                                  (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pSCFVT7-hM21; human; ONS-M21 antibody; chimeric medulloblastoma; brain tumour; treatment; diagnosis; Fv
                                                                                                                                                                                                                                                                                                                                                                              WO9514041-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ONS-M21 antibody Fv fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR76682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR76682 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 vss 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 gvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpadgntky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 OVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyvn----qdywgqgttvt 133
                                                                                                                                                                                                                                         Sato K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                             93JP-0291078
                                                                                                                                                                                                                                                                                                                        94WO-JP01763
                                                                                                                                                                                                                                                                                                                                                                                                   /note= "FLAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140..154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= sig_peptide
23..139
                                                                                                                                                                                                                                                                                                                                                                                                                 262..269
                                                                                                                                                                                                                                                                                                                                                                                                                              /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                            155..269
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "heavy variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                         Tsuchiya M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "linker"
                                                                                                                                                                                                                                                                                                                                                                                                                          "light variable region"
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4; Mismatches
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ches 10;
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                                                                                                                                                         has low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fragment.
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The present sequence is a scFv (ragment from the chimaeric human/murine monoclonal antibody (MAD) OMS-M21. The MAD was prepd. by combining light and heavy variable region DNA, from a murine anti-human myeloblastoma cell MAD, with human light and heavy constant region sequences, respectively to produce chimaeric human/murine light and heavy chain DNA mols. A recombinant vector for the expression of the heavy and light chain DNA mols. was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                      Example 6; Pages 40-41; 45pp; Japanese.
                                                                                                                                                                   treatment of cerebral tumours, e.g. myeloblastoma
                                                                                                                                                                                Reshaped anti-human mycloblastoma cell human antibody - has low human antigenicity, and is therefore useful for diagnosis and
                                                                                                                                                                                                                                            N-PSDB; AAT38662
                                                                                                                                                                                                                                                                                                                           18-OCT-1994;
19-NOV-1993;
                                                                                                                                                                                                                                                              WPI; 1996-358509/36
                                                                                                                                                                                                                                                                                          (CHUS ) CHUGAI PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                          18-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                        JP08169900-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine; human; myeloblastoma; chimaera; monoclonal antibody; chimera; single stranded Fv region; low human antigenicity; diagnosis; treatment; cerebral tumour; reshaped.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimaeric human/murine MAb ONS-M21 scFv fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpadgntky 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 OVOLVOSGAEVKKPGASVKVSCKASGFNIKDTYLHWVROAPGORLEWNGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                       94JP-0252166
93JP-0291078
                                                                                                                                                                                                                                                                                                                                                                     94JP-0285057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- FLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label - linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "heavy variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "light variable region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 523; DB 16;
Pred. No. 1.9e-40;
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PAN XXXX PAN X PAN XXXX PAN XXXX PAN XXXX XXX XXX PAN XXX XXX XXX XXX PAN XXX XXX PAN XXX XXX PAN XXX XXX PAN XXX XXX PAN XXX XXX PAN XXX XXX PAN XXX XXX PAN XXX XXX PAN XXX XXX PAN XXX XXX PAN XXX

The sequence encodes the mouse antibody 21.6 heavy chain variable region, Hc, directed against leukocyte adhesion molecule VAA-4. Cloned are linked to human constant regions in the construction of a humanized antibody against VAA-4. The 5 and 3 ends of the mouse CDNAs are constant regions in the construction of a humanized modified using PCR primers (See AAQ99893-98) and then subcloned into constant regions. In the humanized light than Aappa or gamma-1. L58 and 5. In the humanized light than a mino acids L5.

Claim 13; Page 70; 105pp; English.

inilammatory disease.

for treating

by the amino acid present in the equivalent position of the mouse

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                                                                                                                                                              New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                            WPI; 1995-269276/35.
                                                                                                                                                                                                                                        Bendig MM,
                                                                                                                                                                                                                                                           (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                       25-JAN-1994;
                                                                                                                                                                                                                                                                                                              25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                        27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                 W09519790-A1
                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                 Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanized VLA-4 antibody 21.6 heavy chain variable region, Hc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR81325 standard; Protein; 119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR81325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepd, and used to transform a host cell. The host cell was then cultured, and the expression prods. of the heavy and light chain DNA mois. sepd and connected with a peptide linker to produce a single stranded by region. The reshaped by region has low human antigenicity, and is therefore expected to be useful as an agent for the diagnosis and treatment of cerebral tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 VSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 qvqlvqsgaevkkpgssvkvsckasgfnikdtylhwvrqapgqglewmgridpadgntky 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103;
                                                                                                                                                                                                                                    Jones TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                    94US-0186269
                                                                                                                                                                                                                                                                                                           95WO-US01219
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83.7%;
                                                                                                                                                                                                                                 Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 523; DB 17;
Pred. No. 1.9e-40;
                                                                                                                                                                                                                               Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transfected into COS cells. The humanized antibodies can be used for inhibiting adhesion of a leukocyte to an endothelial cell and for treating inflammatory diseases such as multiple sclerosis. The can also be used in the treatment of stroke, corebrat transas, meningits or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating detecting VLA-4, for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-idiotype antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                        asthma; atheroscierosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW22426 standard; Protein; 119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                           acute leukocyte mediated lung injury; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                           atopic dermatitis; psoriasis; myocardial ischaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised alpha-4 integrin antibody 21.6 VH HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-DEC-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                   Chimeric synthetic
                                                                                                                                                                                                                                                                                                                                                                                   Chimeric Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                Chimeric Mus musculus;
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                                                                                                                                                                                                                                                                           Misc-difference
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                                                                                                                                                                      Region
                                                                                                                                                                                                                 Region
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                               Misc-difference 72
                                                                              Region
                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 sqkfqgrvtitadtsastaymelsslrsedtavyycarggyfgs----gsnywgqgtlvt 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DEKEOGRYTITADISASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLYT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 qvqlvqsgaevkkpgasvkvsckasgfniksyamhwvrqapgqrlewmgwinagngntky 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                /note= "21/28'CL framework region 1" 27..30
                                                                                                                                                                          /note= "\overline{21.6} complementarity determining region 1" 36..49
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "\bar{2}1.6 complementarity determining region 2" 67..98
                                                                                                                                                                                                                                                                 /note-
/note= "21/28'CL Arg-72 is substd. by Ala of mouse 21.6 VL, important in supporting the CDR2
                                                 /note= "21/28'CL framework region 3"
                                                                                                                                           /note= "21/28'CL framework region 2"
                                                                                                                                                           /label- FR2
                                                                  /label= FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.6%;
                                                                                                                                                                                                                                                                 *21/28'CL residues 27-30 are replaced by
                                                                                                                                                                                                                                        binding.
                                                                                                                                                                                                                                                     those of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 515; DB 16; Length 119; pred. No. 4.1e-40;
                                                                                                                                                                                                                                                     MAb 21.6, involved in antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Uses of humanised alpha-4 integrin antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9718838-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          region (see AAM22410) of mouse alpha a throw, The contains an 21/26 for and a modified human 21/28 for framework the comparison to additional amino acid substitution (TYP102Phe) is comparison to additional amino acid substitution (TYP102Phe) is comparison to 21.6 yH and VL regions are used to produce chained humanised 21.6 21.6 yH and VL regions are used to produce chained humanised 21.6 yH and VL regions are used to produce chained humanised 21.6 yH and VL regions are used to produce chained humanised 21.6 yH and VL regions at the manufacture of amedicament for treating antibodies useful in the manufacture of amedicament for treating antibodies useful in the manufacture of a medicament for a modification, graft to the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Fig 7; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The humanised antibodies have a half-life in the human circulation essentially equivalent to that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     composed of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          naturally
117 vss 119
                                                      121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                            61 sqkfqgrvtitadtsastaymelsslrsedtavyycarggyfgs----gsnywgqgtlvt 116
                                                                                                                                                                      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                 1 qvqlvqsgaevkkpgasvkvsckasgfniksyamhwvrqapgqrlewmgwinagngntky 60
                                                                                                                                                                                                                                                                                               1 OVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               olypeptide, designated Hc. comprises the heavy chain variable (VH) of a humanised alpha-4 integrin antibody 216. It is ed to complementarity determining regions (CDRs) from the VH (see ANN 2440) of mouse alpha-4 integrin monocional antibody (see ANN 2440) of mouse alpha-4 integrin monocional antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      occurring human antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones ST, Leger OJ,
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US18807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113..123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99..112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= FR4
                                                                                                                                                                                                                                                                                                                                                                                           78.6%; Score 515; DB 18; 82.9%; Pred. No. 4.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               loop"
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                                                                                                                                                                                                                                                                                                                                                                      Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 119;
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